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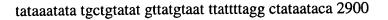
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agac 154

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<210> 19 <211> 457 <212> PRT <213> Homo sapiens

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Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp Ala Gly Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu . 445 Leu Arg Asn Arg Asp Phe Ser <210> 20 <211>24 <212> DNA

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<211> 285 <212> PRT <213> Homo sapiens

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Ala Leu Leu Gly Thr Pro Val Gly Gly Leu Leu Met Ala Phe Gln

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<220> <221> unsure <222> 262, 330, 371 <223> unknown base

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<220> <223> Synthetic oligonucleotide probe

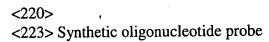
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<210> 33 <211> 20 <212> DNA <213> Artificial Sequence



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<210> 34 <211> 40 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 35 <211> 1819 <212> DNA <213> Homo sapiens

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Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu 170 175 180

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Pro Arg Ala Asn Pro Ser Ala Phe Leu 200

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<220> <221> unsure <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336 <223> unknown base

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gttgtgcccc acttgc 566

<210> 39 <211> 264 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 84-85, 206 <223> unknown base

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<210> 40 <211> 21 <212> DNA <213> Artificial Sequence

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<213> Homo sapiens

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<211> 359 <212> PRT <213> Homo sapiens

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Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser 35 40 45

Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe 50 55 60

Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val 65 70 75

Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe 80 85 90

Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp 95 100 105

Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly 110 115 120

Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys 125 130 135

Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro 140 145 150

Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val 155 160 165

Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala 170 175 180

Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys 185 190 195

Leu Pro Leu Gln Arg Ser Ala Ala Arg Leu Leu Phe Ser Phe Tyr

Lys Asp Gly Arg Ile Val Gln Ser Arg Gly Leu Ser Ser Glu Phe Gln Ile Pro Thr Ala Ser Glu Asp His Ser Gly Ser Tyr Trp Cys Glu Ala Ala Thr Glu Asp Asn Gln Val Trp Lys Gln Ser Pro Gln Leu Glu Ile Arg Val Gln Gly Ala Ser Ser Ala Ala Pro Pro Thr Leu Asn Pro Ala Pro Gln Lys Ser Ala Ala Pro Gly Thr Ala Pro Glu Glu Ala Pro Gly Pro Leu Pro Pro Pro Pro Thr Pro Ser Ser Glu Asp Pro Gly Phe Ser Ser Pro Leu Gly Met Pro Asp Pro His Leu Tyr His Gln Met Gly Leu Leu Leu Lys His Met Gln Asp Val Arg Val Leu Leu Gly His Leu Leu Met Glu Leu Arg Glu Leu Ser Gly His Gln Lys Pro Gly Thr Thr Lys Ala Thr Ala Glu <210>46 <211>18 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>46 tgggctgtgt cctcatgg 18

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<213> Homo sapiens

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Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe 200 205 210
Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile 215 220 225
Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys 230 235 240
Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser245250255
Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr 260 265 270
Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe 275 280 285
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Met Ala Tyr Ile Met Leu Cys Arg Lys Thr Ser Gln Gln Glu His 305 310 315
Val Tyr Glu Ala Ala Arg 320
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<220> <223> Synthetic oligonucleotide probe
<400> 53 tatccctcca attgagcacc ctgg 24
<210> 54 <211> 21
<212> DNA <213> Artificial Sequence
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<400> 54 gtcggaagac atcccaacaa g 21

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<220> <223> Synthetic oligonucleotide probe

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<400> 59

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Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp 35 40 45

Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln505560

Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu 65 70 75

Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu808590

Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp 95 100 105

Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val 110 115 120

Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro 125 130 135

Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr 140 145 150

Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr 155 160 165

Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro 170 175 180

Pro Lys Ser Arg Ile Asp Tyr Asn His Pro Gly Arg Val Leu Leu 185 190 195
Gln Asn Leu Thr Met Ser Tyr Ser Gly Leu Tyr Gln Cys Thr Ala 200 205 210
Gly Asn Glu Ala Gly Lys Glu Ser Cys Val Val Arg Val Thr Val 215 220 225
Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly 230 235 240
Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu 245 250 255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro 260 265 270
Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val 275 280 285
Lys Pro Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly 290 295 300
Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln 305 310 315
Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr 320 325 330
Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro 335 340 345
Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro 350 355 360
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<223> Synthetic oligonucleotide probe

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<210>61 <211>24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 61 actaggctgt atgcctgggt gggc 24

<210> 62 <211>43 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 62 gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43.

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tctccccgcc tgggcggcct cgccgctggg caggtgctga gcgcccctag 150

agecteeett geegeeteee teetetgeee ggeegeagea gtgeacatgg 200

ggtgttggag gtagatgggc tcccggcccg ggaggcggcg gtggatgcgg 250

cgctgggcag aagcagccgc cgattccagc tgccccgcgc gccccgggcg 300

<213> Homo sapiens

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	230	235	240		
Val Pro	Ser Ser Thr Ty 245	yr Val Pro Lys 250	Gly Met Asn Ser Thr Glu 255		
Ser Asn	Ser Ser Ala Se 260	er Val Arg Pro 265	Lys Val Leu Ser Ser Ile 270		
Gln Glu	Gly Thr Val F 275	Pro Asp Asn Tl 280	nr Ser Ser Ala Arg Gly Lys 285		j
Glu Asp	Val Asn Lys' 290	Thr Leu Pro A 295	sn Leu Gln Val Val Asn His 300		
Gln Gln	Gly Pro His H 305	lis Arg His Ile 310	Leu Lys Leu Leu Pro Ser 315		 •
Met Glu	1 Ala Thr Gly (320	Gly Glu Lys Se 325	er Ser Thr Pro Ile Lys Gly 330		
Pro Lys	Arg Gly His F 335	Pro Arg Gln As 340	n Leu His Lys His Phe Asp 345		
Ile Asn	Glu His Leu P 350	ro Trp Met Ile 355	Val Leu Phe Leu Leu Leu 360		·
Val Leu	Val Val Ile V 365	al Val Cys Ser 370	Ile Arg Lys Ser Ser Arg 375		
Thr Leu	Lys Lys Gly I 380	Pro Arg Gln As 385	sp Pro Ser Ala Ile Val Glu 390		
Lys Ala	Gly Leu Lys I 395	Lys Ser Met Th 400	nr Pro Thr Gln Asn Arg Glu 405	· ·	
Lys Trp	lle Tyr Tyr Cy 410	ys Asn Gly His 415	s Gly Ile Asp Ile Leu Lys 420		
Leu Val	l Ala Ala Gln 425	Val Gly Ser Gl 430	n Trp Lys Asp lle Tyr Gln 435		
Phe Leu	ı Cys Asn Ala 440	Ser Glu Arg G 445	ilu Val Ala Ala Phe Ser Asn 450		
Gly Tyr	Thr Ala Asp	His Glu Arg A	la Tyr Ala Ala Leu Gln His		

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	455	460	465
Trp Thr	Ile Arg Gly Pr	o Glu Ala Ser	Leu Ala Gln Leu Ile Ser
	470	475	480
Ala Leu	Arg Gln His A	Arg Arg Asn A	sp Val Val Glu Lys Ile Arg
	485	490	495
Gly Leu	Met Glu Asp	Thr Thr Gln L	eu Glu Thr Asp Lys Leu Ala
	500	505	510
Leu Pro	Met Ser Pro S	er Pro Leu Se	r Pro Ser Pro Ile Pro Ser
	515	520	525
Pro Asn	Ala Lys Leu (Glu Asn Ser A	la Leu Leu Thr Val Glu Pro
	530	535	540
Ser Pro	Gln Asp Lys A	Asn Lys Gly Pl	he Phe Val Asp Glu Ser Glu
	545	550	555
Pro Leu	Leu Arg Cys	Asp Ser Thr S	er Ser Gly Ser Ser Ala Leu
	560	565	570
Ser Arg	Asn Gly Ser I	Phe Ile Thr Lys	s Glu Lys Lys Asp Thr Val
	575	580	585
Leu Arg	g Gln Val Arg	Leu Asp Pro C	Cys Asp Leu Gln Pro Ile Phe
	590	595	600
Asp As	p Met Leu His	Phe Leu Asn	Pro Glu Glu Leu Arg Val Ile
	605	610	615
Glu Glu	1 Ile Pro Gln A	la Glu Asp Ly	rs Leu Asp Arg Leu Phe Glu
	620	625	630
Ile Ile C	Bly Val Lys Se	r Gln Glu Ala	Ser Gln Thr Leu Leu Asp
	635	640	645
Ser Val	Tyr Ser His L 650	eu Pro Asp Le 655	eu Leu
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<220> <223> Synthetic oligonucleotide probe

<400> 65 gtagcagtgc acatggggtg ttgg 24

<210> 66 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 66 accgcacatc ctcagtctct gtcc 24

<210> 67 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 67 acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68 <211> 2412 <212> DNA <213> Homo sapiens

<400> 68 atgggaagcc agtaacactg tggcctacta tctcttccgt ggtgccatct 50

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ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200

ataagteetg ttgcaccaga tgcagatget gttgetgeac agateetgte 250

actgctgcca ttgaagtttt ttccaatcat cgtcattggg atcattgcat 300

tgatattagc actggccatt ggtctgggca tccacttcga ctgctcaggg 350 aagtacagat gtcgctcatc ctttaagtgt atcgagctga tagctcgatg 400 tgacggagtc tcggattgca aagacgggga ggacgagtac cgctgtgtcc 450 gggtgggtgg tcagaatgcc gtgctccagg tgttcacagc tgcttcgtgg 500 aagaccatgt gctccgatga ctggaagggt cactacgcaa atgttgcctg 550 tgcccaactg ggtttcccaa gctatgtgag ttcagataac ctcagagtga 600 gctcgctgga ggggcagttc cgggaggagt ttgtgtccat cgatcacctc 650 ttgccagatg acaaggtgac tgcattacac cactcagtat atgtgaggga 700 gggatgtgcc tctggccacg tggttacctt gcagtgcaca gcctgtggtc 750 atagaagggg ctacagctca cgcatcgtgg gtggaaacat gtccttgctc 800 tcgcagtggc cctggcaggc cagcettcag ttccaggget accacetgtg 850 cgggggctct gtcatcacgc ccctgtggat catcactgct gcacactgtg 900 tttatgactt gtacctcccc aagtcatgga ccatccaggt gggtctagtt 950 tccctgttgg acaatccagc cccatcccac ttggtggaga agattgtcta 1000 ccacagcaag tacaagccaa agaggctggg caatgacatc gcccttatga 1050 agetggeegg gecaeteacg tteaatgaaa tgatecagee tgtgtgeetg 1100 cccaactctg aagagaactt ccccgatgga aaagtgtgct ggacgtcagg 1150 atggggggcc acagaggatg gaggtgacgc ctcccctgtc ctgaaccacg 1200 cggccgtccc tttgatttcc aacaagatct gcaaccacag ggacgtgtac 1250 ggtggcatca tctccccctc catgctctgc gcgggctacc tgacgggtgg 1300 cgtggacagc tgccaggggg acagcggggg gcccctggtg tgtcaagaga 1350 ggaggctgtg gaagttagtg ggagcgacca gctttggcat cggctgcgca 1400 gaggtgaaca agcctggggt gtacacccgt gtcacctcct tcctggactg 1450

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<210> 69 <211> 453 <212> PRT <213> Homo sapiens <400>69

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Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala 20 25 30

Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro 35 40 45

Leu Lys Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile 50 55 60

Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly 65 70 75

Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala 80 85 90

Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr 95 100 105

Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe 110 115 120

Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly125130135

His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr 140 145 150

Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe 155 160 165

Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys 170 175 180

Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala 185 190 195

Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg 200 205 210

Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu 215 220 225

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Ser C	Gln Trp Pro Trp G 230	aln Ala Ser Lei 235	u Gln Phe Gln Gly' 240	Tyr His		
Leu	Cys Gly Gly Ser V 245	/al Ile Thr Pro 250	Leu Trp Ile Ile Thi 255	Ala	۰	
Ala I	His Cys Val Tyr A 260	Asp Leu Tyr Lo 265	eu Pro Lys Ser Trp 270	Thr Ile		
Gln	Val Gly Leu Val S 275	Ser Leu Leu A 280	sp Asn Pro Ala Pro 285	Ser His		
Leu	Val Glu Lys Ile V 290	al Tyr His Ser 295	Lys Tyr Lys Pro L 300	ys Arg	. · ·	
Leu	Gly Asn Asp Ile A 305	Ala Leu Met L 310	ys Leu Ala Gly Pro 315	Leu Thr		
Phe	Asn Glu Met Ile (320	Gln Pro Val Cy 325	ys Leu Pro Asn Ser 330	Glu Glu		
Asn	Phe Pro Asp Gly 335	Lys Val Cys 7 340	Trp Thr Ser Gly Trp 345	Gly Ala		
Thr	Glu Asp Gly Gly 350	Asp Ala Ser P 355	ro Val Leu Asn His 360	s Ala Ala		
Val	Pro Leu Ile Ser A 365	sn Lys Ile Cys 370	Asn His Arg Asp V 375	Val Tyr		
Gly	Gly Ile Ile Ser Pro 380	Ser Met Leu 385	Cys Ala Gly Tyr L 390	eu Thr		·
Gly	Gly Val Asp Ser (395	Cys Gln Gly A 400	sp Ser Gly Gly Pro 405	Leu Val		
Cys	Gln Glu Arg Arg 410	Leu Trp Lys I 415	eu Val Gly Ala Th 420	r Ser Phe		
Gly	Ile Gly Cys Ala G . 425	ilu Val Asn Ly 430	ys Pro Gly Val Tyr 435	Thr Arg		
Val	Thr Ser Phe Leu /	Asp Trp Ile Hi	s Glu Gln Met Glu	Arg Asp		

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Leu Lys Thr

<210> 70 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 70 tgacatcgcc cttatgaagc tggc 24

<210> 71 <211> 24 <212> DNA <213> Artificial Sequence

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<400> 71 tacacgtccc tgtggttgca gatc 24

<210> 72 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 73 <211> 3305 <212> DNA <213> Homo sapiens

<400> 73 cccacgcgtc cgtcctagtc cccgggccaa ctcggacagt ttgctcattt 50

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gaaat 3305

<210> 74 <211> 735 <212> PRT <213> Homo sapiens

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Leu Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu

230 235 240	
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile A 245 250 255	лg
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys 260 265 270	Cys
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu A 275 280 285	Asp
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn 290 295 300	ı Ala
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly M 305 310 315	Лet
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly I 320 325 330	lle
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr 335 340 345	: Leu
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr 350 355 360	r Leu
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly 365 370 375	y Cys
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe S 380 385 390	Ser
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly 395 400 405	Met
Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe 410 415 420	e Gly
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Glu Glu 425 430 435	u Cys
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys As 440 445 450	sn Ala
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly	Leu

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	455	460	465					
Cys Cys	Glu Asp Cys (470	Gln Leu Lys Pr 475	o Ala Gly Th 480	nr Ala Cys Arg	۰ ۰			
Asp Ser	Ser Asn Ser C 485	ys Asp Leu Pro 490	o Glu Phe Cy 495	s Thr Gly Ala		·	•	
Ser Pro	His Cys Pro Al 500	la Asn Val Tyr 505	Leu His Asp 510	Gly His Ser	·			
Cys Gln	Asp Val Asp 515	Gly Tyr Cys Ty 520	yr Asn Gly Il 525	e Cys Gln Thr				
His Glu	Gln Gln Cys V 530	/al Thr Leu Tr 535	p Gly Pro Gly 540	y Ala Lys Pro				
Ala Pro	Gly Ile Cys Ph 545	e Glu Arg Val 550	Asn Ser Ala 555	Gly Asp Pro				
Tyr Gly	Asn Cys Gly I 560	Lys Val Ser Ly 565	s Ser Ser Phe 570	Ala Lys Cys				
Glu Me	t Arg Asp Ala 575	Lys Cys Gly L 580	ys lle Gln Cy 585	s Gln Gly Gly				
Ala Ser	Arg Pro Val II 590	e Gly Thr Asn 595	Ala Val Ser 600	lle Glu Thr				
Asn Ile	Pro Leu Gln G 605	ln Gly Gly Arg 610		Arg Gly Thr				
His Val	Tyr Leu Gly A 620	Asp Asp Met Pi 625	ro Asp Pro G 630	ly Leu Val Leu				
Ala Gly	Thr Lys Cys A 635	Ala Asp Gly Ly 640	vs Ile Cys Leu 645	ı Asn Arg Gln				
Cys Gln	n Asn Ile Ser V 650	al Phe Gly Val 655	l His Glu Cys 660	Ala Met Gln				
Cys His	Gly Arg Gly V 665	√al Cys Asn A 670	sn Arg Lys A 675	sn Cys His Cys				
Glu Ala	His Trp Ala P	ro Pro Phe Cy	s Asp Lys Ph	e Gly Phe Gly				

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680 685 690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln 695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro 710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu lle 725 730 735

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<400>75

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<210> 81 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 82 <211> 19 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 82 cttcgctggg aagagtttg 19

<210> 83 <211> 50 <212> DNA <213> Artificial Sequence

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<210> 84 <211> 1714 <212> DNA <213> Homo sapiens

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<210> 85 <211> 67 <212> PRT <213> Homo sapiens

<400> 85

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65

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<210> 87 <211>29 <212> DNA <213> Artificial Sequence

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<210> 88 <211> 50 <212> DNA <213> Artificial Sequence

<220>

<400> 88

<210> 89 <211>2956 <212> DNA

<400> 89

<213> Homo sapiens

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His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala

Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn 330 325 320 Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe 345 335 340 Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp 360 355 350 Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys 375 365 370 lle Ala Glu Val Asp Cys Thr Ala Glu Arg Asn lle Cys Ser Lys 390 385 380 Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly 405 400 395 Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu 420 415 410 His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu 430 425 <210>91 <211>20 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>91 atgttcttcg cgccctggtg 20 <210>92 <211>21 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>92 ccaagccaac acactctaca g 21

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<213> Homo sapiens

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<210> 102 <211> 730 <212> PRT <213> Homo sapiens

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Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp ·155 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala · 175 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg 230 _____235 Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala

Arg Ile S	Ser His Leu Ly 350	s Ile Leu Gln (355	Cys Gln Gly Phe Tyr Gln 360		
Leu Cys	Gly Val His C 365	Gln Glu Asp V 370	al Ile Tyr Leu Ala Leu Pro 375		
Leu Tyr	His Met Ser G 380	ily Ser Leu Le 385	u Gly Ile Val Gly Cys Met 390	·	
Gly Ile (Gly Ala Thr Va 395	al Val Leu Lys 400	Ser Lys Phe Ser Ala Gly 405		
Gln Phe	Trp Glu Asp (410	Cys Gln Gln H 415	lis Arg Val Thr Val Phe Gli 420	n	
Tyr Ile (Gly Glu Leu C 425	ys Arg Tyr Lei 430	u Val Asn Gln Pro Pro Ser 435		
Lys Ala	Glu Arg Gly I 440	His Lys Val A1 445	rg Leu Ala Val Gly Ser Gly 450		
Leu Arg	g Pro Asp Thr 7 455	Trp Glu Arg P 460	he Val Arg Arg Phe Gly Pr 465	o	
Leu Glr	n Val Leu Glu ' 470	Thr Tyr Gly L 475	eu Thr Glu Gly Asn Val Al 480	a	
Thr Ile .	Asn Tyr Thr G 485	ly Gln Arg Gl 490	y Ala Val Gly Arg Ala Ser 495		• •
Trp Leu	1 Tyr Lys His I 500	le Phe Pro Phe 505	e Ser Leu Ile Arg Tyr Asp 510		
Val Thr	r Thr Gly Glu I 515	Pro Ile Arg Asj 520	p Pro Gln Gly His Cys Met 525	:	,
Ala Thi	r Ser Pro Gly C 530	Glu Pro Gly Le 535	u Leu Val Ala Pro Val Ser 540		
Gln Glr	n Ser Pro Phe I 545	eu Gly Tyr A 550	la Gly Gly Pro Glu Leu Ala 555	à	
Gln Gly		Lys Asp Val P 565	Phe Arg Pro Gly Asp Val Ph 570	he	

Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu 580 585 575 Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu 595 600 590 Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp 610 615 605 Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His 620 625 630 Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His 640 645 635 Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu 655 660 650 Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu 670 675 665 Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn 685 690 680

Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu 695 700 705

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<210>104



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<210> 108 <211> 2579 <212> DNA <213> Homo sapiens

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<210> 109 <211> 555 <212> PRT <213> Homo sapiens

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Asn Asp Met Phe Val Arg Thr Tyr Gly Met Leu Tyr Met Gln Asn Ser Glu Val Phe Gln Asp Leu Phe Thr Glu Leu Lys Arg Tyr Tyr Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys

Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe 350 355 360

Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr 365 370 375

Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu 380 385 390

Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr 395 400 405

Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu 410 415 420

Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile 425 430 435

Met Asn Asp Gly Leu Thr Asn Gln Ile Asn Asn Pro Glu Val Asp 440 445 450

Val Asp Ile Thr Arg Pro Asp Thr Phe Ile Arg Gln Gln Ile Met 455 460 465

Ala Leu Arg Val Met Thr Asn Lys Leu Lys Asn Ala Tyr Asn Gly 470 475 480

Asn Asp Val Asn Phe Gln Asp Thr Ser Asp Glu Ser Ser Gly Ser 485 490 495

Gly Ser Gly Ser Gly Cys Met Asp Asp Val Cys Pro Thr Glu Phe 500 505 510

Glu Phe Val Thr Thr Glu Ala Pro Ala Val Asp Pro Asp Arg Arg 515 520 525

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Trp Ser Leu Thr Cys Ile Val Leu Ala Leu Gln Arg Leu Cys Arg 545 550 555

<210> 110 <211> 21 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400>110 aagcgtgaca gcgggcacgt c 21

<210>111 <211>24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400>111 tgcacagtct ctgcagtgcc cagg 24

<210>112 <211>40 <212> DNA <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400>112 gaatgetgga acgggcacag caaagecaga tacttgeetg 40

<210>113 <211>4649 <212> DNA

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aataagttag ctgagaaaac gcacgcagtt tgcagcgcct gcgccgggtg 100

tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgctgcccgg agtttctgcg gaggtggagg gagatcagga aacggcttct 250

cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150

<213> Homo sapiens

<400>113

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acgcatatgg tcggaaaatg gcacttgggt tttaacagaa aagaatgcat 1450 gcccaccaga agaggatttg ataccttttt tggttccctt ttgggaagtg 1500 gggattacta tacacactac aaatgtgaca gtcctgggat gtgtggctat 1550 gacttgtatg aaaacgacaa tgctgcctgg gactatgaca atggcatata 1600 ctccacacag atgtacactc agagagtaca gcaaatctta gcttcccata 1650 accccacaaa gcctatattt ttatatactg cctatcaagc tgttcattca 1700 ccactgcaag ctcctggcag gtatttcgaa cactaccgat ccattatcaa 1750 cataaacagg agaagatatg ctgccatgct ttcctgctta gatgaagcaa 1800 tcaacaacgt gacattggct ctaaagactt atggtttcta taacaacagc 1850 attatcattt actcttcaga taatggtggc cagcctacgg caggagggag 1900 taactggcct ctcagaggta gcaaaggaac atattgggaa ggagggatcc 1950 gggctgtagg ctttgtgcat agcccacttc tgaaaaacaa gggaacagtg 2000 tgtaaggaac ttgtgcacat cactgactgg taccccactc tcatttcact 2050 ggctgaagga cagattgatg aggacattca actagatggc tatgatatct 2100 gggagaccat aagtgagggt cttcgctcac cccgagtaga tattttgcat 2150 aacattgacc cctatacacc aaggcaaaaa atggctcctg ggcagcaggc 2200 tatgggatet ggaacaetge aatecagtea gecateagag tgeageaetg 2250 gaaattgett acaggaaate etggetacag egaetgggte ecceetcagt 2300 ctttcagcaa cctgggaccg aaccggtggc acaatgaacg gatcaccttg 2350 tcaactggca aaagtgtatg gcttttcaac atcacagccg acccatatga 2400 gagggtggac ctatctaaca ggtatccagg aatcgtgaag aagctcctac 2450 ggaggctctc acagttcaac aaaactgcag tgccggtcag gtatcccccc 2500 aaagacccca gaagtaaccc taggctcaat ggaggggtct ggggaccatg 2550 gtataaagag gaaaccaaga aaaagaagcc aagcaaaaat caggctgaga 2600 aaaagcaaaa gaaaagcaaa aaaaagaaga agaaacagca gaaagcagtc 2650 tcaggtaaac cagcaaattt ggctcgataa tatcgctggc ctaagcgtca 2700 ggcttgtttt catgctgtgc cactccagag acttctgcca cctggccgcc 2750 acactgaaaa ctgtcctgct cagtgccaag gtgctactct tgcaagccac 2800 acttagagag agtggagatg tttatttctc tcgctccttt agaaaacgtg 2850 gtgagteetg agtteeactg etgtgettea gteaactgae caaacaetge 2900 tttgaattat aggaggagaa caataaccta ccatccgcaa gcatgctaat 2950 ttgatggaag ttacagggta gcatgattaa aactaccttt gataaattac 3000 agtcaaagat tgtgtcacct caaaggcctt gaagaatata ttttcttggt 3050 gaatttttgt atgtctgtca tatgacactt gggtttttta attaattcta 3100 ttttatatat ataaatatat gtttcttttc ctgtgaaaag ctgtttttct 3150 cacatgtgaa cagcttgcac ctcattttac catgcgtgag ggaatggcaa 3200 ataagaatgt ttgagcacac tgcccacaat gaatgtaact attttctaaa 3250 cactttacta gaagaacatt tcagtataaa aaacctaatt tattttaca 3300 gaaaaatatt ttgttgtttt tataaaaagt tatgcaaatg acttttattt 3350 caagcactgt aatactataa attaatgtaa tactgtgtga attcagacta 3450 taaaaaacat cattcagaaa actttataat cgtcattgtt caatcaagat 3500 tttgaatgta ataagatgaa tatatteett acaaattaet tggaaattea 3550 atgtttgtgc agagttgaga caactttatt gtttctatca taaactattt 3600 atgtatetta attattaaaa tgatttaett tatggeaeta gaaaatttae 3650 tgtggctttt ctgatctaac ttctagctaa aattgtatca ttggtcctaa 3700

aaaataaaaa tetttactaa taggcaattg aaggaatggt ttgctaacaa 3750 ccacagtaat ataatatgat tttacagata gatgcttccc cttggctatg 3800 acatggagaa agattttccc ataataataa ctaatattta tattaggttg 3850 gtgcaaaact agttgcggtt tttcccatta aaagtaataa ccttactctt 3900 atacaaagtg gacactgtgg ggagatacag agaaatggaa gatacggatc 3950 ctgcctggag taggtaacct tgcttggaaa ccccacatgc aaacgtcatg 4000 aggagaatta aaggagtatt atcagtaatg aagtttatca tgggtcatca 4050 atgagcatag attggtgtgg atcctgtaga ccctggtgtt ttctttgaag 4100 tgccctctcc taatgcagag gccttgaagc ttacagtata cacttgaaaa 4150 gtcacagata gctagaatta tgatctttga agttataact gtgatctgaa 4200 aatgtgtgtg gtggtatgac agcataccat taaatacatt tacatcacag 4250 ctcaaaggac tgtgatataa tccatttata tcacaactca aaggactgtg 4300 atataatcca tttatatcac agctcacagt ttctgaaaat gtataaaaga 4350 atctataatc tagtactgaa attactaaat tgggtaagat gatttaaatg 4400 atagtgtaaa gttgtatttc ctaaagtttg tgttttgtcg acagtatctt 4500

<210> 114 <211> 515 <212> PRT <213> Homo sapiens

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Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln

·	230	235	240			
Met Tyr	r Thr Gln Arg 245	g Val Gln Glr 250	n Ile Leu Ala Ser 255	His Asn Pro		
The İ wa	Dro To Dhe I	ou Tyr Thr	Ala Tyr Gln Ala '	Val His Ser		
	260	265	270			
Pro Leu			Phe Glu His Tyr	Arg Ser Ile		
	275	280	. 285			
Ile Asn	Ile Asn Arg A 290	Arg Arg Tyr 295	Ala Ala Met Leu 300	Ser Cys Leu		
Asp Gi	305	310	Leu Ala Leu Ly 315			• •
Phe Tyr	r Asn Asn Se	r lle lle lle Ty	yr Ser Ser Asp As	sn Gly Gly	-	
	320	325	330			
Gln Pro	o Thr Ala Gly 335	Gly Ser Asn 340	Trp Pro Leu Arg 345	g Gly Ser Lys		
	`			Dha Wal Hia	·	·
Gly Th	350	355	Arg Ala Val Gly 360			
Ser Pro	Leu Leu Lys		y Thr Val Cys Ly	s Glu Leu Val		
	365	370	375			
His Ile '	Thr Asp Trp 380	Tyr Pro Thr 1 385	Leu Ile Ser Leu A 390	la Glu Gly		
				le Tro Glu		
Gin lie	395	400	Asp Gly Tyr Asp 405			
Thr Ile	Ser Glu Gly		Pro Arg Val Asp	Ile Leu His		
	410	415	420			
Asn Ile	Asp Pro Tyr 425	Thr Pro Arg 430	Gln Lys Met Ala 435	Pro Gly Gln		
Gln Ala	a Met Gly Sei 440	r Gly Thr Leu 445	u Gln Ser Ser Glr 450	Pro Ser Glu		
Cys Ser	r Thr Gly Asr	n Cys Leu Gli	n Glu Ile Leu Ala	Thr Ala Thr		

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460 465 455 Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly 475 480 470 Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe 485 490 495 Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr 510 505 500 Gly Ile Gln Glu Ser 515 <210>115 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>115 cccaacccaa ctgtttacct ctgg 24 <210>116 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>116 ctctctgagt gtacatctgt gtgg 24 <210>117 <211> 53 <212> DNA <213> Artificial Sequence <220>

<223> Synthetic oligonucleotide probe

<220>





<221> unsure <222> 33 <223> unknown base

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cgg 53

<210> 118 <211> 2260 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 2009, 2026, 2033, 2055, 2074, 2078, 2086 <223> unknown base

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gtaataataa 2260

<210> 119 <211> 338 <212> PRT <213> Homo sapiens

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	95	100	105
Gln His .	Arg Cys Val A	sn Thr His Gl	y Ser Tyr Lys Cys Phe Cys
	110	115	120
Leu Ser (Gly His Met L	eu Met Pro As	p Ala Thr Cys Val Asn Ser
	125	130	135
Arg Thr	Cys Ala Met I	le Asn Cys Gli	n Tyr Ser Cys Glu Asp Thr
	140	145	150
Glu Glu	Gly Pro Gln C	Cys Leu Cys Pr	o Ser Ser Gly Leu Arg Leu
	155	160	165
Ala Pro J	Asn Gly Arg A	Asp Cys Leu A	sp lle Asp Glu Cys Ala Ser
	170	175	180
Gly Lys	Val Ile Cys Pr	o Tyr Asn Arg	Arg Cys Val Asn Thr Phe
	185	190	195
Gly Ser	Гуг Tyr Cys L	ys Cys His Ile	Gly Phe Glu Leu Gln Tyr
	200	205	210
Ile Ser G	ily Arg Tyr As	p Cys Ile Asp	Ile Asn Glu Cys Thr Met
	215	220	225
Asp Ser	His Thr Cys S	er His His Ala	Asn Cys Phe Asn Thr Gln
	230	235	240
Gly Ser 1	Phe Lys Cys L	ys Cys Lys Gl	n Gly Tyr Lys Gly Asn Gly
	245	250	255
Leu Arg	Cys Ser Ala I	le Pro Glu Asn	Ser Val Lys Glu Val Leu
	260	265	270
Arg Ala	•		g Ile Lys Lys Leu Leu Ala 285
	275	280	
His Lys .			a Lys Ile Lys Asn Val Thr 300
·	Asn Ser Met L 290	Lys Lys Lys Al 295	a Lys Ile Lys Asn Val Thr

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• .

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Gly Lys Lys Gly Asn Glu Glu Lys 335

<210> 120 <211> 22 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 120 cctcagtggc cacatgctca tg 22

<210> 121 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 121 ggctgcacgt atggctatcc atag 24

<210> 122 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 122 gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123 <211> 1199 <212> DNA <213> Homo sapiens

<400> 123 gggagctgct gctgtggctg ctggtgctgt gcgcgctgct cctgctcttg 50 gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100 ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150 tgtgggtgac tggagcctcg agtggaattg gtgaggagct ggcttaccag 200 ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcatga 250 gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300 aagatatact tgttttgccc cttgacctga ccgacactgg ttcccatgaa 350 gcggctacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400 caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450 atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500 acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550 tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600 actgtgctag caagcatgct ctccggggtt tttttaatgg ccttcgaaca 650 gaacttgcca catacccagg tataatagtt tctaacattt gcccaggacc 700 tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750 ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800 gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850 ctcagaacaa cctttcttgt tagtaacata tttgtggcaa tacatgccaa 900 cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950 tttaagagtg gtgtggatgc agactettet tattttaaaa tetttaagae 1000 aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050 aatggaaaac atgaaaacag caatcttctt atgcttctga ataatcaaag 1100 actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150 gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199



<210> 124 <211> 289 <212> PRT <213> Homo sapiens

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Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser 20 25 30

Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu 35 40 45

- Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu 50 55 60
- Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val 65 70 75
- Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly 80 85 90
- Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr 95 100 105
- Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr 110 115 120
- Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile 125 130 135
- Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser 140 145 150
- Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn155160165
- Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser 170 175 180
- Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser 185 190 195

Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln 200 205 210

Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile 215 220 225

Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro 230 235 240

Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala 245 250 255

Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe260265270

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys 275 280 285

Thr Lys His Asp

<210> 125 <211> 19 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 125 gcaatgaact gggagctgc 19

<210> 126 <211> 19 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 126 ctgtgaatag catcctggg 19

<210> 127 <211> 20





<212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 127 cttttcaagc cactggaggg 20

<210> 128 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 128 ctgtagacat ccaagctggt atcc 24

<210> 129 <211> 23 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 129 aagagtctgc atccacacca ctc 23

<210> 130 <211> 46 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 130 acctgacgct actatgggcc gagtggcagg gacgacgccc agaatg 46

<210> 131 <211> 2365 <212> DNA <213> Homo sapiens

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Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe 35 40 45

Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn 50 55 60

Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln657075

Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val 80 85 90

Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu 95 100 105

Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu 110 115 120

Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro 125 130 135

Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu 140 145 150

Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln

Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro Glu Thr Pro Glu Met Ser Asp Glu Asp Ser Cys Val Ala Cys Gly Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys Phe lle Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly

	380	385	390
Ala Tyr '	Thr His Pro G	lu Gly Gly Tyr	Asp Met Ala Leu Leu Leu
	395	400	405
Leu Ala	Gln Pro Val T	hr Leu Gly Ala	a Ser Leu Arg Pro Leu Cys
	410	415	420
Leu Pro	Tyr Pro Asp H	lis His Leu Pro	Asp Gly Glu Arg Gly Trp
	425	430	435
Val Leu	Gly Arg Ala A	arg Pro Gly Al	a Gly Ile Ser Ser Leu Gln
	440	445	450
Thr Val	Pro Val Thr L	eu Leu Gly Pro	o Arg Ala Cys Ser Arg Leu
	455	460	465
His Ala	Ala Pro Gly G	ly Asp Gly Sei	Pro Ile Leu Pro Gly Met
	470	475	480
Val Cys	Thr Ser Ala V	al Gly Glu Leu	1 Pro Ser Cys Glu Gly Leu
	485	490	495
Ser Gly	Ala Pro Leu V	al His Glu Val	Arg Gly Thr Trp Phe Leu
	500	505	510
Ala Gly	Leu His Ser P	he Gly Asp Al	a Cys Gln Gly Pro Ala Arg
	515	520	525
Pro Ala	Val Phe Thr A	la Leu Pro Ala	a Tyr Glu Asp Trp Val Ser
	530	535	540
Ser Leu	Asp Trp Gln V	/al Tyr Phe Al	a Glu Glu Pro Glu Pro Glu
	545	550	555
Ala Glu	Pro Gly Ser C	ys Leu Ala As	n Ile Ser Gln Pro Thr Ser
	560	565	570
Cys			· · ·

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<220> <223> Synthetic oligonucleotide probe

<400> 133 cctgtgctgt gcctcgagcc tgac 24

<210> 134 <211> 24 <212> DNA <213> Artificial Sequence

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<400> 134 gtgggcagca gttagcaccg cctc 24

<210> 135 <211> 45 <212> DNA <213> Artificial Sequence

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<210> 136 <211> 1998 <212> DNA <213> Homo sapiens

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<210> 137 <211> 316 <212> PRT <213> Homo sapiens

<220> <221> unsure <222> 233 <223> unknown amino acid

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Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu 65 70 75

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala 80 85 90

Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala 95 100 105

Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe 110 115 120

Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser125130135

Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu 140 145 150

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys 155 160 165

Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp 170 175 180

Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met 185 190 195

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val 200 205 210

Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro 215 220 225

Val Leu Gln Gln Asp Ala His Xaa Ser Val Thr Ile Thr Gly Gln 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu 245 250 255

Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys 260 265 270

Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala 275 280 285



Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln 290 295 300

Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile 305 310 315

Ala

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<220> <223> Synthetic oligonucleotide probe

<400> 139 gctgtctgtc tgtctcattg 20

<210> 140 <211> 20 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 140 ggacacagta tactgaccac 20

<210> 141 <211> 24 <212> DNA

<213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 141 tgcgaaccag gcagctgtaa gtgc 24

<210> 142 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 142 tggaagaaga gggtggtgat gtgg 24

<210> 143 <211> 45 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 143 cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144 <211> 2336 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 1620, 1673 <223> unknown base

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tacgttetta aatetatgaa gtegagggae etttegetge ttttgtaggg 150 acttctttcc ttgcttcagc aacatgaggc ttttcttgtg gaacgcggtc 200 ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250 agtgaaaatt gaagttetee agaageeatt catetgeeat egeaagaeea 300 aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350 ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400 gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggcttga 450 aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500 ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550 atttaatatt gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600 cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650 gttaaagcat atttaaagaa ggagtttgaa aaacatggtg cggtggtgaa 700 tgaaagtcat catgatgctt tggtggagga tatttttgat aaagaagatg 750. aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800 gagttataga gatacatcta cccttttaat atagcactca tctttcaaga 850 gagggcagtc atctttaaag aacattttat ttttatacaa tgttctttct 900 tgctttgttt tttattttta tatatttttt ctgactccta tttaaagaac 950 cccttaggtt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000 aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050 acagatatga agctttgttt tactttctca cttataaatt taaaatgttg 1100 caactgggaa tataccacga catgagacca ggttatagca caaattagca 1150 ccctatattt ctgcttccct ctattttctc caagttagag gtcaacattt 1200 gaaaagcctt ttgcaatagc ccaaggcttg ctattttcat gttataatga 1250

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Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly 35 40 45

Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly 50 55 60

Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro lle 65 70 75

Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln 80 85 90

Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu lle lle 95 100 105

Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro 110 115 120

Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg 125 130 135

Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn 140 145 150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys 155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His 170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys 185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu

Leu

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<220>

<223> Synthetic oligonucleotide probe

<400> 146 ctttccttgc ttcagcaaca tgaggc 26

<210> 147 <211> 25 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 147 gcccagagca ggaggaatga tgagc 25

<210> 148 <211> 49 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 149 <211> 2196 <212> DNA <213> Homo sapiens

<400> 149 aataaagctt ccttaatgtt gtatatgtct ttgaagtaca tccgtgcatt 50

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<210> 154 <211> 23 <212> DNA <213> Artificial Sequence

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<400> 154 gcacgtttct cagcatcacc gac 23

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Trp Leu Asn Leu Glu Leu Leu Pro Val Ile Ile Asp Cys Trp Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys Thr Phe Ser Leu Glu Phe Leu Asp Pro Ser Lys Ser Ser Val Gly Ser Tyr Phe His Thr Met Val Glu Ser Leu Val Gly Trp Gly Tyr Thr Arg Gly Glu Asp Val Arg Gly Ala Pro Tyr Asp Trp Arg Arg Ala Pro Asn Glu Asn Gly Pro Tyr Phe Leu Ala Leu Arg Glu Met Ile Glu Glu Met Tyr Gln Leu Tyr Gly Gly Pro Val Val Leu Val Ala His Ser Met Gly Asn Met Tyr Thr Leu Tyr Phe Leu Gln Arg Gln Pro Gln Ala Trp Lys Asp Lys Tyr Ile Arg Ala Phe Val Ser Leu Gly Ala Pro Trp Gly Gly Val Ala Lys Thr Leu Arg Val Leu Ala Ser Gly Asp Asn Asn Arg Ile Pro Val Ile Gly Pro Leu Lys Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln

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Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu 305 310 315 Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys 330 320 325 Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu 335 340 345 Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp 350 355 360 Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln 365 370 375 Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser 385 390 380 Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu 395 400 405 Lys Arg Val Leu Leu Gly Pro 410 <210>158 <211>23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>158 ctggggctac acacggggtg agg 23 <210>159 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe

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Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly 50 55 60

Val Leu Crp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val 65 70 75

Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe 80 85 90

Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu 95 100 105

Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser Thr110115120

Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly 125 130 135

Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro 140 145 150

Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu 155 160 165

Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val 170 175 180

Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile 185 190 195

Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu

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Leu Lys	Gly Pro Asp H	lis Leu Ala Ser	Ser Cys Leu Trp His Leu		
	230	235	240		
Gln Gly	Pro Lys Asp L	eu Met Leu Ly	vs Leu Arg Leu Glu Trp Thr		
	245	250	255		
Leu Ala	Glu Cys Arg A	Asp Arg Leu A	la Met Tyr Asp Val Ala Gly		
	260	265	270		
Pro Leu	Glu Lys Arg L	eu lle Thr Ser	Val Tyr Gly Cys Ser Arg		
	275	280	285		
Gln Glu	Pro Val Val G	lu Val Leu Ala	a Ser Gly Ala Ile Met Ala		
	290	295	300		
Val Val	Trp Lys Lys G	ly Leu His Ser	Tyr Tyr Asp Pro Phe Val		
	305	310	315		
Leu Ser	Val Gln Pro V	al Val Phe Glr	n Ala Cys Glu Val Asn Leu		
	320	325	330		
Thr Leu	Asp Asn Arg	Leu Asp Ser G	In Gly Val Leu Ser Thr Pro		
	335	340	345		
Tyr Phe	Pro Ser Tyr Ty	yr Ser Pro Gln	Thr His Cys Ser Trp His		
	350	355	360		
Leu Thr	Val Pro Ser L	eu Asp Tyr Gly	y Leu Ala Leu Trp Phe Asp		
	365	370	375		
Ala Tyr	Ala Leu Arg A	Arg Gln Lys Ty	rr Asp Leu Pro Cys Thr Gln		
	380	385	390		
Gly Gln	Trp Thr Ile Gl	n Asn Arg Arg	g Leu Cys Gly Leu Arg Ile		
	395	400	405		
Leu Gln	Pro Tyr Ala C	ilu Arg Ile Pro	Val Val Ala Thr Ala Gly		
	410	415	420		
lle Thr lle Asn Phe Thr Ser Gln lle Ser Leu Thr Gly Pro Gly					

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425 430 435

Val Arg Val His Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro 440 445 450

Gly Glu Phe Leu Cys Ser Val Asn Gly Leu Cys Val Pro Ala Cys 455 460 465

Asp Gly Val Lys Asp Cys Pro Asn Gly Leu Asp Glu Arg Asn Cys 470 475 480

Val Cys Arg Ala Thr Phe Gln Cys Lys Glu Asp Ser Thr Cys lle 485 490 495

Ser Leu Pro Lys Val Cys Asp Gly Gln Pro Asp Cys Leu Asn Gly 500 505 510

Ser Asp Glu Glu Gln Cys Gln Glu Gly Val Pro Cys Gly Thr Phe 515 520 525

Thr Phe Gln Cys Glu Asp Arg Ser Cys Val Lys Lys Pro Asn Pro530535540

Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly Ser Asp Glu Glu 545 550 555

His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg lle Val Gly 560 565 570

Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu 575 580 585

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp 590 595 600

Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met 605 610 615

Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln 620 625 630

Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu 635 640 645

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650 655 660

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- Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro 710 715 720
- Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg 725 730 735
- Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln 740 745 750
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- tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

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<400> 172 taatccagca gtgcaggccg gg 22

<210> 173 <211> 50 <212> DNA <213> Artificial Sequence

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Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu 50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu 65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His 80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu 95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val 110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val 125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp 140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu 155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn 170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala 185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro

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Phe Gly	Leu Ser Ile Gl	y Ile Gln Met l	Pro Val Gly His Ile Asp		
	230	235	240		
lle Tyr P	ro Asn Gly Gl	y Asp Phe Gln	Pro Gly Cys Gly Leu Asn		
	245	250	255		
Asp Val	Leu Gly Ser I	e Ala Tyr Gly	Thr Ile Thr Glu Val Val		
	260	265	270		
Lys Cys	Glu His Glu A	Arg Ala Val Hi	s Leu Phe Val Asp Ser Leu		
	275	280	285		
Val Asn	Gln Asp Lys 1	Pro Ser Phe Al	a Phe Gln Cys Thr Asp Ser		
	290	295	300		
Asn Arg	Phe Lys Lys (Gly Ile Cys Let	u Ser Cys Arg Lys Asn Arg		
	305	310	315		
Cys Asn	Ser Ile Gly T	yr Ásn Ala Lys	s Lys Met Arg Asn Lys Arg		
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Gly Asn Leu Gln Ser Leu Glu Cys Pro 350					
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<220> <223> Synthetic oligonucleotide probe

<210>181 <211>44 <212> DNA <213> Artificial Sequence

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<213> Artificial Sequence

<212> DNA

<400>180

<220> <223> Synthetic oligonucleotide probe

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100

95

Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro Gly Leu Thr Pro Arg Pro Val Pro Ser Leu Pro Cys Asn Val Thr Leu Glu Asp Phe Tyr Gly Val Phe Ser Ser Pro Gly Tyr Thr His Leu Ala Ser Val Ser His Pro Gln Ser Cys His Trp Leu Leu Asp Pro His Asp Gly Arg Arg Leu Ala Val Arg Phe Thr Ala Leu Asp Leu Gly Phe Gly Asp Ala Val His Val Tyr Asp Gly Pro Gly Pro Pro Glu Ser Ser Arg Leu Leu Arg Ser Leu Thr His Phe Ser Asn Gly Lys Ala Val Thr Val Glu Thr Leu Ser Gly Gln Ala Val Val Ser Tyr His Thr Val Ala Trp Ser Asn Gly Arg Gly Phe Asn Ala Thr Tyr His Val Arg Gly Tyr Cys Leu Pro Trp Asp Arg Pro Cys Gly Leu Gly Ser Gly Leu Gly Ala Gly Glu Gly Leu Gly Glu Arg

Cys Tyr Ser Glu Ala Gln Arg Cys Asp Gly Ser Trp Asp Cys Ala Asp Gly Thr Asp Glu Glu Asp Cys Pro Gly Cys Pro Pro Gly His Phe Pro Cys Gly Ala Ala Gly Thr Ser Gly Ala Thr Ala Cys Tyr Leu Pro Ala Asp Arg Cys Asn Tyr Gln Thr Phe Cys Ala Asp Gly Ala Asp Glu Arg Arg Cys Arg His Cys Gln Pro Gly Asn Phe Arg Cys Arg Asp Glu Lys Cys Val Tyr Glu Thr Trp Val Cys Asp Gly Gln Pro Asp Cys Ala Asp Gly Ser Asp Glu Trp Asp Cys Ser Tyr Val Leu Pro Arg Lys Val Ile Thr Ala Ala Val Ile Gly Ser Leu Val Cys Gly Leu Leu Leu Val Ile Ala Leu Gly Cys Thr Cys Lys Leu Tyr Ala lle Arg Thr Gln Glu Tyr Ser lle Phe Ala Pro Leu Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser Tyr Gly Gln Leu lle Ala Gln Gly Ala lle Pro Pro Val Glu Asp Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu Arg Ser Leu Clu Clu Ile Leu Arg Glu Asp Met Thr Pro Gly Gly Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg

Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp Val Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu Ala Glu Asp Glu Pro Leu Leu Thr <210> 184 <211>20 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>184 ggctgtcact gtggagacac 20 <210>185

<211> 18 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 185 gcaaggtcat tacagctg 18

<210> 186 <211> 23 <212> DNA <213> Artificial Sequence

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<210> 187 <211> 23 <212> DNA <213> Artificial Sequence

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Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr

45 40 35 lle Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile 60 50 55 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe 70 75 65 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe 90 80 85 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr 100 105 95 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys 120 115 110 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn 130 135 125 Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu 145 150 140

Val Leu

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<220> <221> unsure <222> 78, 212, 234, 487 <223> unknown base

<400> 191

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<210> 196 <211> 518 <212> PRT <213> Homo sapien

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Gly Ser Gly Thr Asn Gly Gly Ser Leu Val Leu Gly Gly Ile Glu Pro Ser Leu Tyr Lys Gly Asp Ile Trp Tyr Thr Pro Ile Lys Glu Glu Trp Tyr Tyr Gln Ile Glu Ile Leu Lys Leu Glu Ile Gly Gly Gln Ser Leu Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala lle Val Asp Ser Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser Glu

Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly 470 475 480

Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Leu Pro Phe Arg 485 490 495

Cys Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu Ser 500 505 510

Ser Leu Val Arg His Arg Trp Lys 515

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<220> <223> Synthetic oligonucleotide probe

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<210> 198 <211> 19 <212> DNA <213> Artificial Sequence

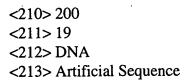
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<210> 199 <211> 20 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 199 ggatgtagcc agcaactgtg 20



<220> <223> Synthetic oligonucleotide probe

<400> 200 gccttggctc gttctcttc 19

<210> 201 <211> 18 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 201 ggtcctgtgc ctggatgg 18

<210> 202 <211> 22 <212> DNA <213> Artificial Sequence

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<400> 202 gacaagacta cctccgttgg tc 22

<210> 203 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 203 tgatgcacag ttcagcacct gttg 24

<210> 204





<211> 47 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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cgcctccgcc ttcggaggct gacgcgcccg ggcgccgttc caggcctgtg 50

<210> 205 <211> 1939 <212> DNA <213> Homo sapiens

<400> 205

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taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaa 1939

<210> 206 <211> 377 <212> PRT <213> Homo sapiens

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Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly 20 25 30

Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn 35 40 45

Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly 50 55 60

Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala 65 70 75

Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile 80 85 90

Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe 95 100 105

Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile 110 115 120

His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe 125 130 135

Asn Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr 140 145 150

His Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val 155 160 165

Val Val Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe 170 175 180

Lys Arg Leu Asp Arg Pro Val Val Gly Trp Arg Gln Glu Leu Arg

185 190 195

Ala Tyr A	la Asp Thr Ly	vs Leu Ala Asn	a Val Leu Phe Ala Arg Glu				
	200	205	210				
Leu Ala A	Asn Gln Leu G	lu Ala Thr Gly	y Val Thr Cys Tyr Ala Ala				
	215	220	225				
His Pro G	Hy Pro Val As	n Ser Glu Leu	Phe Leu Arg His Val Pro				
	230	235	240				
Gly Trp L	eu Arg Pro Le 245	eu Leu Arg Pro 250	255 Leu Ala Trp Leu Val Leu				
Arg Ala I	Pro Arg Gly G	ly Ala Gln Thi	Pro Leu Tyr Cys Ala Leu				
	260	265	270				
Gln Glu (Gly Ile Glu Pro	Leu Ser Gly	Arg Tyr Phe Ala Asn Cys				
	275	280	285				
His Val C	Glu Glu Val Pr	o Pro Ala Ala	Arg Asp Asp Arg Ala Ala				
	290	295	300				
His Arg I	Leu Trp Glu A	la Ser Lys Arg	, Leu Ala Gly Leu Gly Pro				
	305	310	315				
Gly Glu A	Asp Ala Glu P	ro Asp Glu As	sp Pro Gln Ser Glu Asp Ser				
	320	325	330				
Glu Ala Pro Ser Ser Leu Ser Thr Pro His Pro Glu Glu Pro Thr335340345							
Val Ser C	Gln Pro Tyr Pr	o Ser Pro Gln	Ser Ser Pro Asp Leu Ser				
	350	355	360				
Lys Met	Thr His Arg Il	e Gln Ala Lys	Val Glu Pro Glu Ile Gln				
	365	370	375				
Leu Ser							

<210> 207 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe

<400> 207 cttcatggcc ttggacttgg ccag 24

<210> 208 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 208 acgccagtgg cctcaagctg gttg 24

<210> 209 <211> 45 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 209 ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210 <211> 3716 <212> DNA <213> Homo sapiens

<400> 210

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caageetcag gecageeace teceaceate egetggttge tgaatgggea 200

gcccctgagc atggtgcccc cagacccaca ccacctcctg cctgatggga 250

cccttctgct gctacagccc cctgcccggg gacatgccca cgatggccag 300

gccctgtcca cagacctggg tgtctacaca tgtgaggcca gcaaccggct 350 tggcacggca gtcagcagag gcgctcggct gtctgtggct gtcctccggg 400 aggatttcca gatccagcct cgggacatgg tggctgtggt gggtgagcag 450 tttactctgg aatgtgggcc gccctggggc cacccagagc ccacagtctc 500 atggtggaaa gatgggaaac ccctggccct ccagcccgga aggcacacag 550 tgtccggggg gtccctgctg atggcaagag cagagaagag tgacgaaggg 600 acctacatgt gtgtggccac caacagcgca ggacataggg agagccgcgc 650 agcccgggtt tccatccagg agccccagga ctacacggag cctgtggagc 700 ttctggctgt gcgaattcag ctggaaaatg tgacactgct gaacccggat 750 cctgcagagg gccccaagcc tagaccggcg gtgtggctca gctggaaggt 800 cagtggccct gctgcgcctg cccaatctta cacggccttg ttcaggaccc 850 agactgcccc gggaggccag ggagctccgt gggcagagga gctgctggcc 900 ggctggcaga gcgcagagct tggaggcctc cactggggcc aagactacga 950 gttcaaagtg agaccateet etggeegge tegaggeeet gacageaacg 1000 tgctgctcct gaggctgccg gaaaaagtgc ccagtgcccc acctcaggaa 1050 gtgactctaa agcctggcaa tggcactgtc tttgtgagct gggtcccacc 1100 acctgctgaa aaccacaatg gcatcatccg tggctaccag gtctggagcc 1150 tgggcaacac atcactgcca ccagccaact ggactgtagt tggtgagcag 1200 acccagctgg aaatcgccac ccatatgcca ggctcctact gcgtgcaagt 1250 ggctgcagtc actggtgctg gagctgggga gcccagtaga cctgtctgcc 1300 tccttttaga gcaggccatg gagcgagcca cccaagaacc cagtgagcat 1350 ggtccctgga ccctggagca gctgagggct accttgaagc ggcctgaggt 1400 cattgccacc tgcggtgttg cactctggct gctgcttctg ggcaccgccg 1450

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Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu 35 40 45

Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu 50 55 60

Leu Pro Asp Gly Thr Leu Leu Leu Gln Pro Pro Ala Arg Gly 65 70 75

His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr 80 85 90

Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly95100105

Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln 110 115 120

Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu 125 130 135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp 140 145 150

Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val 155 160 165

Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu 170 175 180

Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu 185 190 195

Ser Arg	Ala Ala Arg V 200	Val Ser Ile Gln (205	Glu Pro Gln Asp Tyr T 210	hr	1	
Glu Pro	Val Glu Leu L 215	Leu Ala Val Arg 220	g Ile Gln Leu Glu Asn 225	Val		
Thr Leu	Leu Asn Pro A 230	Asp Pro Ala Gl 235	lu Gly Pro Lys Pro Arg 240	Pro		
Ala Val	Trp Leu Ser T 245	Trp Lys Val Ser 250	Gly Pro Ala Ala Pro A 255	la		
Gln Ser	Tyr Thr Ala L 260	eu Phe Arg Th 265	r Gln Thr Ala Pro Gly 270	Gly		
Gln Gly	Ala Pro Trp A 275	Ala Glu Glu Lev 280	u Leu Ala Gly Trp Gln 285	Ser		
Ala Giu	1 Leu Gly Gly I 290	Leu His Trp Gl 295	y Gln Asp Tyr Glu Phe 300	Lys		
Val Arg	g Pro Ser Ser G 305	Gly Arg Ala Arg 310	g Gly Pro Asp Ser Asn 315	Val		
Leu Lei	u Leu Arg Leu 320	Pro Glu Lys Va 325	al Pro Ser Ala Pro Pro 330	Gln		
Glu Va	1 Thr Leu Lys I 335	Pro Gly Asn Gl 340	ly Thr Val Phe Val Ser 345	Trp		
Val Pro	Pro Pro Ala C 350	Glu Asn His Ası 355	n Gly Ile Ile Arg Gly T 360	yr	•	• .
Gln Va	l Trp Ser Leu (365	Gly Asn Thr Se 370	r Leu Pro Pro Ala Asn 375	Тгр		٤
Thr Va	l Val Gly Glu (380	Gln Thr Gln Le 385	eu Glu Ile Ala Thr His M 390	vlet		
Pro Gly	y Ser Tyr Cys V 395	Val Gln Val Ala 400	a Ala Val Thr Gly Ala (405	Gly		
Ala Gly	y Glu Pro Ser A 410	Arg Pro Val Cys 415	s Leu Leu Leu Glu Gln 420	Ala		

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Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr 425 430 435	
Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala 440 445 450	
Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Gly Thr Ala Val 455 460 465	
Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly 470 475 480	
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met 485 490 495	
Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr 500 505 510	
Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Leu Ser Ser Arg 515 520 525	
Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu 530 535 540	
Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp 545 550 555	
Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser 560 565 570	
Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu 575 580 585	
Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp 590 595 600	
Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu 605 610 615	
Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Gln Glu Leu Gln 620 625 630	
His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu 635 640 645	

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Leu Arg Ala Cys	Glu Leu Gly As	n Arg Gly Ser Lys Asn Le	u Ser		
650	655	660			
Gln Ser Pro Gly A 665	Ala Val Pro Gln 670	Ala Leu Val Ala Trp Arg 675	Ala		
Leu Gly Pro Lys 680	Leu Leu Ser Ser 685	Ser Asn Glu Leu Val Thr 690	Arg		
His Leu Pro Pro A 695	Ala Pro Leu Phe 700	Pro His Glu Thr Pro Pro 7 705	ſhr		
Gln Ser Gln Gln 710	Thr Gln Pro Pro 715	Val Ala Pro Gln Ala Pro S 720	Ser	•	
Ser Ile Leu Leu P 725	Pro Ala Ala Pro I 730	le Pro Ile Leu Ser Pro Cys 735			
Ser Pro Pro Ser F 740	Pro Gln Ala Ser S 745	Ser Leu Ser Gly Pro Ser Pr 750	0		
Ala Ser Ser Arg I 755	Leu Ser Ser Ser S 760	Ser Leu Ser Ser Leu Gly G 765	lu	·	
Asp Gln Asp Ser 770	Val Leu Thr Pro 775	o Glu Glu Val Ala Leu Cy 780	s Leu		
Glu Leu Ser Glu 785	Gly Glu Glu Th 790	Pro Arg Asn Ser Val Ser 795	Pro		
Met Pro Arg Ala 800	Pro Ser Pro Pro 805	Thr Thr Tyr Gly Tyr lle S 810	er	•	
Val Pro Thr Ala 815	Ser Glu Phe Thr 820	Asp Met Gly Arg Thr Gly 825	Gly		
Gly Val Gly Pro 830	Lys Gly Gly Val 835	Leu Leu Cys Pro Pro Arg 840	Pro		
Cys Leu Thr Pro 845	Thr Pro Ser Glu 850	Gly Ser Leu Ala Asn Gly 855	Тгр		
Gly Ser Ala Ser (860	Glu Asp Asn Ala 865	Ala Ser Ala Arg Ala Ser 870	Leu		

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Val Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala 880 875 885 Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu 900 890 895 Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro 910 915 905 Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro 920 925 930 Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser 940 945 935 His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp 950 955 960 Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro 970 975 965 Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser 980 985 <210>212

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<220> <223> Synthetic oligonucleotide probe

<400> 212 gaagggacct acatgtgtgt ggcc 24

<210> 213 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 213 actgacette cagetgagee acae 24 <210> 214 <211> 50 <212> DNA <213> Artificial Sequence

<223> Synthetic oligonucleotide probe

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<220>

<400>214

<210> 215 <211> 2749 <212> DNA

<220>

<221> unsure <222> 1869, 1887 <223> unknown base

<213> Homo sapiens

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gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttcte 200
tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250
agggcagggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300
accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggt 350
cgaaaaacgg ggccccgatg agtctttact gatctctct tc00
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Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp 35 40 45

His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg 50 55 60

Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Glu Gly Gln Glu Thr Met 65 70 75

Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu 80 85 90

Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr95100105

Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile 110 115 120

Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser 125 130 135

Pro Thr Phe Gin Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala 140 145 150

Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu 155 160 165

Tyr Pro Ála Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu 170 175 180

Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr 185 190 195

Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro 200 205 210

Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala 215 220 225 Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg 240 230 235 Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu 250 245 255 Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His 260 270 265 Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln 275 280 285 Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys 290 295 300 Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro 305 310 315 Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val 320 325 330

Ser Ala

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Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln 65 70 75

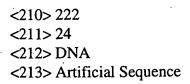
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Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu 95 100 105

Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln 110 115 120

Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys 125 130 135

Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe 140 145



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gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200 gatgtgcaag cggaacctgg aagtcatgga ctcggtgcgc cgcggtgccc 250 agetggeeat tgaggagtge cagtaceagt teeggaaceg gegetggaae 300 tgctccacac tcgactcctt gcccgtcttc ggcaaggtgg tgacgcaagg 350 gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400 ttgcagtgac gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450 gacaggacag tgcatggggt cagcccacag ggcttccagt ggtcaggatg 500 ctctgacaac atcgcctacg gtgtggcctt ctcacagtcg tttgtggatg 550 tgcgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600 cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650 atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700 gagccgtgcc gcccttccgc caggtgggtc acgcactgaa ggagaagttt 750 gatggtgcca ctgaggtgga gccacgccgc gtgggctcct ccagggcact 800 ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850 acttggagcc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900 ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950 ctgtgagctg ctgtgctgtg gccgcggctt ccacacggcg caggtggagc 1000 tggctgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050 cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100 ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150 aaacagtete ceaceaceta ecceaagaga taetggttgt atttttgtt 1200 ctggtttggt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250 caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300

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Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser 80 85 90

Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly95100105

Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val110115120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys 125 130 135

Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe 140 145 150

Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe 155 160 165

Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser 170 175 180

Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg 185 190 195

Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly 200 205 210

Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro 215 220 225

Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly 230 235 240

Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu 245 250 255

Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu 260 265 270

Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg 280 275 285 Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser 290 295 300 Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe 305 310 315 His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe 320 325 330 His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val 340 345 335 Glu Leu His Thr Cys Arg 350 <210> 227 <211>23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>227 gctgcagctg caaattccac tgg 23 <210> 228 <211>28 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe

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<210> 229 <211> 41 <212> DNA <213> Artificial Sequence <400>230 cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50 gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100 gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150 aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200 ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250 cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300 gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350 ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400 cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450 cgcgtgaccc agggcttggc tgaagccggc aggggccgtg aggacgtccg 500 cactgagetg tteeggege tggaggeegt gaggeteeag aacaacteet 550 gcgagccgtg ccccacgtcg tggctgtcct tcgagggctc ctgctacttt 600 ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650 tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggcttcc 700 tcactcggaa cacgcgtggc cgtggttact ggctgggcct gagggctgtg 750 cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800 cagetteage caetggaace agggagagee caatgaeget tgggggegeg 850

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Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr 95 100 105

Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu 110 115 120

Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala 125 130 135

Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg 140 145 150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys 155 160 165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser 170 175 180

Val Pro Lys Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp 185 190 195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly 200 205 210

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Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val 230 235 240

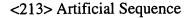
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Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr 260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp 275 280 285

Ile Cys Glu Lys Arg His Asn Cys 290

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<210> 234 <211> 50 <212> DNA <213> Artificial Sequence

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<210> 236 <211> 331 <212> PRT <213> Homo sapiens

<400>236

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		ys Glu Ile Glu 110	u Ala Ala Gly 115	Glu Ala Leu Gln 3 120	Ser Val			
		al Phe Ser Al 125	a Pro Ala Val 1 130	Pro Ser Gly Thr G 135	ily Gln		•	
		la Glu Leu Gl 140	u Val Gln Arg 145	Arg His Ser Leu 150	Val Ser			
		al Arg Ile Val 155	l Pro Ser Pro A 160	Asp Trp Phe Val C 165	ily Val	. 1		
	-	eu Asp Leu C 170	ys Asp Gly As 175	sp Arg Trp Arg Gl 180	u Gln Ala			
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		er Ser Pro Asi 200	n Phe Ala Thr 205	Ile Pro Gln Asp T 210	hr Val			
		e Thr Ser Ser 215	Ser Pro Ser H 220	is Pro Ala Asn Se 225	r Phe			•
:		ro Arg Leu Ly 230	ys Ala Leu Pro 235	Pro Ile Ala Arg V 240	al Thr			
		Arg Leu Arg G 245	iln Ser Pro Arg 250	g Ala Phe Ile Pro I 255	Pro Ala			
		eu Pro Ser Ar 260	g Asp Asn Glu 265	a Ile Val Asp Ser A 270	Ala Ser	•		
		lu Thr Pro Le 275	u Asp Cys Glu 280	i Val Ser Leu Trp 285	Ser Ser			
		eu Cys Gly G 290	ly His Cys Gly 295	Arg Leu Gly Thr 300	Lys Ser			
	÷	arg Tyr Val An 305	rg Val Gln Pro 310	Ala Asn Asn Gly 315	y Ser Pro		- ·	
	-	ilu Leu Glu G 320	lu Glu Ala Glu 325	a Cys Val Pro Asp 330	Asn Cys			

· ·

Val

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<220> <223> Synthetic oligonucleotide probe

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Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly

Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile

Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala

Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr Arg Arg Glu Lys Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met Arg Glu Lys Lys Glu Arg Arg <210> 246 <211>24 <212> DNA <213> Artificial Sequence <220>

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230 235 240

Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser 245 250 255

Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val 260 265 270

Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp 275 280 285

Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala 290 295 300

Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp 305 310 315

Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser 320 325 330

Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His 335 340 345

Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile 350 355 360

Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala 365 370 375

Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg 380 385 390

Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg 395 400 405

Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp 410 415 420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro 425 430 435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu 440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn

465 455 460 Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp 480 470 475 Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met 490 485 495 Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr 510 505 500 Ala His Tyr His Arg Glu Thr Pro Met Met Gly lle Cys Pro Ala 515 520 525 Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu 530 535 540 Pro Gln Glu Trp Ala 545 <210> 255 <211>23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 255 aggtgcctgc aggagtcctg ggg 23 <210> 256 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 256 ccacctcagg aagccgaaga tgcc 24 <210> 257 <211>45 <212> DNA

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Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp 50 55 60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr 65 70 75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe 80 85 90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile 95 100 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val 110 115 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe 125 130 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp 140 145 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly 155 160 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro 170 175 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu 185 190 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys 200 205 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro 215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser 230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val 245 250 255 Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg 260 265 270

Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro 275 280 285

Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val 290 295 300

Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly 305 310 315

Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala 320 325 330

Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln 335 340 345

Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu 350 355 360

His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser 365 370 375

Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu 380 385 390

Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile 395 400 405

Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile 410 415 420

Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe 425 430 435

Ser Arg His Ser Thr lle Leu Asp Tyr lle Asn Val Val Pro Thr 440 445 450

Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn 455 460 465

Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser 470 475 480 Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu 485 490 495

Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu 500 505 510

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atttaaa 2857

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Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser505560

His His Ile Gly Gln Leu Arg Ser Asp Leu Asp Asn Gly Asn Asn 65 70 75

Ser Phe Gin Tyr Lys Leu Leu Gly Ala Gly Ala Gly Ser Thr Phe 80 85 90

Ile Ile Asp Glu Arg Thr Gly Asp Ile Tyr Ala Ile Gln Lys Leu95100105

Asp Arg Glu Glu Arg Ser Leu Tyr Ile Leu Arg Ala Gln Val Ile 110 115 120

Asp Ile Ala Thr Gly Arg Ala Val Glu Pro Glu Ser Glu Phe Val 125 130 135

Ile Lys Val Ser Asp Ile Asn Asp Asn Glu Pro Lys Phe Leu Asp140145150

Glu Pro Tyr Glu Ala Ile Val Pro Glu Met Ser Pro Glu Gly Thr 155 160 165

Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser 170 175 180

Gly Asn Asn Ala Arg Leu Leu Tyr Ser Leu Leu Gln Gly Gln Pro 185 190 195

Tyr Phe Ser Val Glu Pro Thr Thr Gly Val Ile Arg Ile Ser Ser200205210

Lys Met Asp Arg Glu Leu Gln Asp Glu Tyr Trp Val Ile Ile Gln 215 220 225

Ala Lys Asp Met Ile Gly Gln Pro Gly Ala Leu Ser Gly Thr Thr 230 235 240

Ser Val Leu Ile Lys Leu Ser Asp Val Asn Asp Asn Lys Pro Ile 245 250 255 Phe Lys Glu Ser Leu Tyr Arg Leu Thr Val Ser Glu Ser Ala Pro Thr Gly Thr Ser Ile Gly Thr Ile Met Ala Tyr Asp Asn Asp Ile 275 -Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe lle Lys lle Gln Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly Thr lle Thr Thr Ser Asn Ser Leu Asp Arg Glu lle Ser Ala Trp Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu

Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr 710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser 725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu 740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly 755 760 765

Ser Ala Val Gln Ser Asn Asn 770

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<210> 266 <211> 25 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe

<400> 266 cttgactgtc tctgaatctg caccc 25

<210> 267 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 267 aagtggtgga agcctccagt gtgg 24

<210> 268 <211> 52 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 268 ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269 <211> 2747 <212> DNA <213> Homo sapiens

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cttcatctgt aagcggtggt ttgtaattcc tgatcttccc acctcacagt 2600

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<210> 270 <211> 211 <212> PRT <213> Homo sapiens

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp 20 25 30

Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala 35 40 45

Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly 50 55 60

Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser 65 70 75

Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly lle Leu Leu808590

Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met 95 100 105

Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val 110 115 120

Ile Gly Gly Ala Ile Phe Leu Leu Ala Gly Leu Ala Ile Leu Val 125 130 135

Ala Thr Ala Trp Tyr Gly Asn Arg Ile Val Gln Glu Phe Tyr Asp 140 145 150

Pro Met Thr Pro Val Asn Ala Arg Tyr Glu Phe Gly Gln Ala Leu

.

155 160 165

Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu Leu Gly Gly Ala 170 175 180

Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser Tyr Pro Thr 185 190 195

Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys Asp Tyr 200 205 210

Val

<210> 271 <211> 564 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 21, 69, 163, 434, 436, 444 <223> unknown base

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gctgttcctg tccc 564

<210> 272 <211> 498 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 30, 49, 102, 141, 147, 171, 324-325, 339-341 <223> unknown base

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<210> 273 <211> 552 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394 <223> unknown base <400> 273 gggcccgacc attatccaac cgggntcact gttggctcat ctccctctg 50 gatgaancgc gccatentea gaeteeetge eccatggaga tttnneetat 100 getggegaca acatentgae ecceageeat gtaegagggg etttgaaegt 150 engegtgteg eagancaeeg ggeagateea gtgeaaagte tttgaeteet 200 tgetgaatet gngeageaea ttgeageaae eentgeeetg atggtggttg 250 geateeteet gggagtgata geaatetttg tggeeaeegt tggeatgaag 300 tgtatgaagt gettggaaga egatgaggtg eagaagatga ggatggetgt 350 eattggggge gegatatte ttettgeagg tetggetatt innngttgee 400 acageatggt atggeaatag aategtteaa gaattetatg accetatgae 450 eccagteaat geeaggtaeg aatttggtea ggeteette aetggetgg 500 etgetgette tetetgeett etgggaggtg ecctaetttg etgtteetge 550

ga 552

<210> 274 <211> 526 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407 <223> unknown base

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tggaggattn actectatge tggegacaae ategtgacee eccaggeeat 100 ttacegaggg getttggatg tentgentgt egcagageae eggeeagate 150 eccagtgeaaa gtetttgact eettgetgaa tetgageage acattgeaag 200 eaaceegtge ettgatgggg ttggeateet eetgggagtg atageaacet 250 ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttgttg 350 caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400 cnngnnntct atgaccetat gaccecagte aatgecaggt acgaatttgg 450 tcaggetete tteaetgget gggetgetge tteteetgg 500 gtgccetaet ttgetgttee tgteee 526

<210> 275 <211> 398 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274 <223> unknown base

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<221> unsure <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476 <223> unknown base

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<210> 277 <211> 200 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 34, 87, 138, 147, 163, 165-166, 172 <223> unknown base

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cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100 ccccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278





<211> 542 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 26, 43, 55, 77, 198, 361-362, 391-392, 396 <223> unknown base

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<210> 281 <211> 26 <212> DNA <213> Artificial Sequence

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<400> 281 gtgtcacacg tagtctttcc cgctgg 26

<210> 282 <211> 43 <212> DNA <213> Artificial Sequence

<210> 283 <211> 2285 <212> DNA

<213> Homo sapiens

<220>

<223> Synthetic oligonucleotide probe

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<211> 243 <212> PRT <213> Homo sapiens

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Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val

125 130 135 Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr 140 145 150 Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu 155 160 165 Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val 175 180 170 Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly 190 195 185 Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala 210 200 205 Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu 220 225 215 Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys 240 230 235

Ile Ala Leu

<210> 285 <211> 418 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 40, 53, 68, 119, 134, 177-178, 255 <223> unknown base

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ctggagtcag gacaatggnt cgggctgcag aggnttagaa gcgagggcac 150

cagcagtttt gggtggggag caagggnnga gagaaactct tcagcgaatc 200

cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300 taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350 . ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400

gttaacttta aaatgagc 418

<210> 286 <211> 543 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 73, 97 <223> unknown base

<400> 286

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<220>

<221> unsure <222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242 <223> unknown base

<400> 287

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cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100

catatccatg ggatttaaat ttatcataac catgtgtaaa aagaaattaa 150

tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200

acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250

agttaaaaat gtatagtaac 270

<210> 288 <211> 428 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 35, 116, 129, 197, 278, 294, 297, 349, 351 <223> unknown base

<400> 288 ggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50 gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100 gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150 actgattgac ccagcgcttt ggaaataaat ggcagtgctt tgttcantta 200 aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250 attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300 tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350 ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400

ttggagagtc tggtcatgtg gaggtggg 428

<210> 289 <211> 320 <212> DNA <213> Homo sapiens

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atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100

tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150

gaaataaatg gcagtgcttt gttcacttaa agggaccaag ctaaatttgt 200

attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250

atttaactta tttaatgtat ttcatctcat gttttcttat tgtcacaaga 300

gtacagttaa tgctgcgtgc 320

<210> 290 <211> 609 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441, 447, 481, 513, 532, 584, 598 <223> unknown base

<400> 290 aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50

gaaaccntgn gtaatgccac aatggcatat tgtaaatgtc attttaaaca 100

ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150

cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250

<210> 292 <211> 27 <212> DNA

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<210> 291 <211> 493 <212> DNA <213> Homo sapiens

gtattgctg 609

<400> 291

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<213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 292 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293 <211> 23 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 293 aaccaccaga gccaagagcc ggg 23

<210> 294 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 295 <211> 2530 <212> DNA <213> Homo sapiens

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anotanotan ananotanan antananant anonananan atantagan 100

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gctctgatct cagctgacag tgccctcggg gaccaaacaa gcctggcagg 150

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<210> 296 <211> 413 <212> PRT <213> Homo sapiens

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Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala His Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly Asn Asp Ala Asn Cys Ala Tyr Gly

<210> 297 <211>24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400>297 gcatctgcag gagagagcga aggg 24

<210> 298 <211>24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400>298 catcgttccc gtgaatccag aggc 24

<210> 299 <211>45 <212> DNA <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100

tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150

<210> 300 <211>1869 <212> DNA <213> Homo sapiens

<400> 300

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cctcgtgtgg gggggggcate cagagecggg cagttteetg tgtggaggag 1350 gacatecagg ggeatgteae tteagtggaa gagtggaaat geatgtacae 1400 ccetaagatg eceategege agecetgeaa catttttgae tgeeetaaat 1450 ggetggeaea ggagtggtet eegtgeaeag tgacatgtgg eeagggeete 1500 agataeegtg tggteetetg eategaeeat egaggaatge acaeaggagg 1550 etgtageeea aaaacaaage eeeacataaa agaggaatge ategtaeeea 1600 eteeetgeta taaaeeeaaa gagaaaette eagtegagge eaagttgeea 1650 tggtteaaae aageteaaga getagaagaa ggagetgetg tgteagagga 1700 geeetegtaa gttgtaaaag eacagaetgt tetatatttg aaaetgtttt 1750 gtttaaagaa ageagtgtet eaetggttgt agettteatg ggttetgaae 1800 taagtgtaat eateteacea aagetttttg geteeaaat taaagattga 1850

ttagtttcaa aaaaaaaaa 1869

<210> 301 <211> 525 <212> PRT <213> Homo sapiens

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Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala 80 85 90

Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe 95 100 105

Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser110115120

Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala 125 130 135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp 140 145 150

Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln 155 160 165

Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly 170 175 180

Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln 185 190 195

Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr 200 205 210

Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu 215 220 225

Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser 230 235 240

Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp 245 250 255

Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro 260 265 270

Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala 275 280 285

Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg 290 295 300

- Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly305310315
- Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn320325330
- Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile 335 340 345
- Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro 350 355 360
- Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His 365 370 375
- Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser 380 385 390
- Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu 395 400 405
- Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys 410 415 420
- Met Tyr Thr Pro Lys Met Pro Ile Ala Gln Pro Cys Asn Ile Phe 425 430 435
- Asp Cys Pro Lys Trp Leu Ala Gln Glu Trp Ser Pro Cys Thr Val 440 445 450
- Thr Cys Gly Gln Gly Leu Arg Tyr Arg Val Val Leu Cys Ile Asp 455 460 465
- His Arg Gly Met His Thr Gly Gly Cys Ser Pro Lys Thr Lys Pro 470 475 480
- His Ile Lys Glu Glu Cys Ile Val Pro Thr Pro Cys Tyr Lys Pro 485 490 495
- Lys Glu Lys Leu Pro Val Glu Ala Lys Leu Pro Trp Phe Lys Gln 500 505 510
- Ala Gln Glu Leu Glu Glu Gly Ala Ala Val Ser Glu Glu Pro Ser 515 520 525

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<210> 302 <211> 1533 <212> DNA <213> Homo sapiens





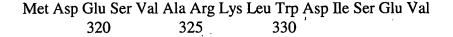
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<210> 303 <211> 336 <212> PRT <213> Homo sapiens

<400> 303

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Leu Arg Gln Ala Ala Glu Cys Gly Pro Glu Pro Gly Val Ser Gly Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg . Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala



Met Val Gly Leu Leu Lys 335

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<220> <221> unsure <222> 20, 34, 62, 87, 221, 229 <223> unknown base

<400> 304

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<210> 306 <211> 26 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 306 gcccatgaca ccaaattgaa gagtgg 26

<210> 307 <211> 45 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 307 aacgcaggga tettecagtg ceettacatg aagaetgaag atggg 45

<210> 308 <211> 1523 <212> DNA <213> Homo sapiens

<400> 308 gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50 cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100

ccagcgcctg teectgteac ggaccccage gttaccatge atectgeegt 150

ctteetatee ttaccegace teagatgete cettetgete etggtaaett 200

gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250

atagatgaaa ttttaaacaa tgctgatgtt gctttagtaa atttttatgc 300

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aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309 <211> 406 <212> PRT <213> Homo sapiens

<400> 309

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Tyr Phe Glu Gln Lys Asp Ser Asp Asn Tyr Arg Val Phe Glu Arg170175180

Val Ala Asn Ile Leu His Asp Asp Cys Ala Phe Leu Ser Ala Phe 185 190 195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile 200 205 210

Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly 215 220 225

Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys 230 235 240

Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu 245 250 255

Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys 260 265 270

Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg 275 280 285

Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp 290 295 300

Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro 305 310 315

Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr 320 325 330

Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys 335 340 345

Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe 350 355 360

His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala 365 370 375

Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu 380 385 390

Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu 395 400 405





Leu

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<220> <221> unsure <222> 36, 48 <223> unknown base

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ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100

caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150

ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311 <211> 598 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396 <223> unknown base

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<210> 313 <211> 19 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 313 gtcagcgatc agtgaaagc 19

<210> 314 <211> 20 <212> DNA <213> Artificial Sequence

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<400> 314 ccagaatgaa gtagctcggc 20



<210> 315 <211> 20 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 315 ccgactcaaa atgcattgtc 20

<210> 316 <211> 19 <212> DNA <213> Artificial Sequence

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<400> 317 ggtgctatag gccaaggg 18

<210> 318 <211> 24 <212> DNA <213> Artificial Sequence

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<210>319





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<210> 321 <211> 1333 <212> DNA <213> Homo sapiens

<400> 321

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tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350

tagaacaaca cacagaagaa ttggtccagt taagtgcatg caaaaagcca 400

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<400> 325 caggaaacag ctatgaccac ctgcacacct gcaaatccat t 41

<210> 326 <211> 20 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 326 gtgcagcaga gtggcttaca 20

<210> 327 <211> 20 <212> DNA <213> Artificial Sequence



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<210> 328 <211> 45 <212> DNA <213> Artificial Sequence

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<210> 330 <211> 323 <212> PRT <213> Homo sapiens

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Leu Phe Ser Ile Cys Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys lle Val lle Phe Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro

Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu 275 280 285

Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg

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<220> <221> unsure <222> 47 <223> unknown base

<213> Homo sapiens

<211> 562 <212> DNA

<210> 332

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actaaattgg aatgtgaatc tgcatgtaca gaagcatatt cccaatctga 200

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatcga 150

gcacacctac cctaaggaag aggagttgta cgcatgtcag agaggttgca 100

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctacccctt 50

<212> DNA <213> Homo sapiens

290

<211> 350

<400> 331

<210> 331

305 · 310 315 Val Asn Leu Ala His Ser Glu Ile 320

Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys

295

300

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<210> 334 <211> 22 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 335 <211> 40 <212> DNA <213> Artificial Sequence <400> 336 gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50 cggcccggag gtgggggcgcc gctggggccg gcccgcacgg gcttcatctg 100 agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150 gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200 gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250 cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300 ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350 ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400 tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450 gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500. ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550 ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600 tctgagtgag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650 attetteaga taacttetgt gaagetgatg acatteagte eetgaaget 700 gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750 accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800 agccacagac aattaaaaga cctttaaatc ctttggcttc tggtcaaggg 850

<210> 336 <211> 1885 <212> DNA <213> Homo sapiens

<400> 335 atggccttgg ccggaggttc ggggaccgct tcggctgaag 40

<220> <223> Synthetic oligonucleotide probe

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<210> 337 <211> 468 <212> PRT

<213> Homo sapiens

<400> 337

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Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln 215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu230235240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His 245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu 260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln275280285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg 290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu lle Glu Leu Arg Ala Leu 305 310 315

Ser Lys Val Leu Pro Phe Phe Glu Arg Pro Asp Phe Gln Leu Phe 320 325 330

Thr Gly Asn Lys Ile Gln Asp Glu Glu Asn Lys Met Leu Leu335340345

Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu His Phe Asp Glu 350 355 360

Asn Ser Phe Phe Ala Gly Asp Lys Lys Glu Ala His Lys Leu Lys 365 370 375

Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile Met Asp 380 385 390

Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln Thr 395 400 405

Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu 410 415 420

Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe His Leu 425 430 435





Thr Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile440445450

Ser Thr Ser Val Lys Glu Leu Glu Asn Phe Arg Asn Leu Leu Gln 455 460 465

Asn Ile His

<210> 338 <211> 507 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 101, 263, 376, 397, 426 <223> unknown base

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tttgctg 507

<210> 339 <211> 20 <212> DNA



<213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 339 aagctgccgg agctgcaatg 20

<210> 340 <211> 21 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 340 ttgcttctta atcctgagcg c 21

<210> 341 <211> 20 <212> DNA <213> Artificial Sequence

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<400> 341 aaaggaggac tttcgactgc 20

<210> 342 <211> 26 <212> DNA <213> Artificial Sequence

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<400> 342 agagattcat ccactgctcc aagtcg 26

<210> 343 <211> 25 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe

<400> 343 tgtccagaaa caggcacata tcagc 25

<210> 344 <211> 50 <212> DNA <213> Artificial Sequence

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aaagagaagt gtggtaaggg aaaatggtct gtgtggaggg gtcaaggagt 600 taaaaaccct agaaagcaaa aggtaggtaa tgtcagggag tagtcttcat 650 gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700 gtaactattt cccccatccc caggcctgtg cccctctctg gtctcgtgct 750 tgtggcagct ctgtcttcag ttctgggata tgtgcccgtg tggatgcttc 800 attccagcct cagggaagcc tggcacccac tgcccaacgt gagccagagg 850 aaggetgagt acttggttee cagaaggaga taetgggtgg gaaaaagatg 900 gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc tatcctcatt 950 gctacctaat gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000 cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050 caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100 catggtgaaa ctccatctct actaaaaaaa aaaaaataca aaaattagct 1150 gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200 ggagactete actteaacee aggaggtgga ggttgeggtg agceaagatt 1250 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400 gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450 agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346 <211> 124 <212> PRT <213> Homo sapiens

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15 5 10 1 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro 20 25 30 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val 45 40 35 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala 50 55 60 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg 70 75 65 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His 85 90 80 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn 95 100 105 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly

Phe Met Val Ser

110

<210> 347 <211> 509 <212> DNA <213> Homo sapiens

<220> <221> unsure <222> 22 <223> unknown base

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115

120

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ggcatggaac tccccttcgt cactcacctg ttcttgcccc tggtgttcct 200

gacaggtete tgetececet ttaacetgga tgaacateae ceaegeetat 250 teeeaggee accagaaget gaatttggat acagtgtett acaacatgtt 300 gggggtggae ageggtggat getggtggge geeeetegg atgggeette 350 aggegaeegg aggggggaeg tttategetg ecetgtaggg ggggeeeaa 400 atgeeeeatg tgeeaaggge caettaggtg actaeeaact gggaaattea 450 teteateetg etgtgaatat geaeetgggg atgtetetgt tagagaeaga 500

tggtgatgg 509

<210> 348 <211> 23 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 349 <211> 24 <212> DNA <213> Artificial Sequence

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<400> 349 caggtgcata ttcacagcag gatg 24

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<210> 351 <211> 2056 <212> DNA <213> Homo sapiens

<400> 351

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actggccctg tttgcctttg ttggcttcat gctgatcctt gtggtcgtgc 1000 cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050 gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150 ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250 aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300 gagcctgttg tctacaagtc tagaagcaac catcagaggc agggtggttt 1350 gtctaacaga acactgactg aggcttaggg gatgtgacct ctagactggg 1400 ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcatccctt 1450 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550 tacacccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650 gatcaaggac tctacacact gggtggcttg gagagcccac tttcccagaa 1700 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000 aaaaaa 2056

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- Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp 20 25 30
- Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser 35 40 45
- Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro505560
- Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu 65 70 75
- Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser 80 85 90
- Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala 95 100 105
- Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln110115120
- Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser125130135
- Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe140145150
- His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe 155 160 165
- Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val 170 175 180
- Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met 185 190 195

Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys 200 205 210

Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu 215 220 225

Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe 230 235 240

Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp 245 250 255

Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val 260 265 270

Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile 275 280 285

Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met 290 295 300

Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser 305 310

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<220> <221> unsure <222> 654, 711, 748, 827 <223> unknown base

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tagaceteag etceaacata tgeattetga agaaagatgg etgagatgae 150

agaatgettt attttggaaa gaaacaatgt tetaggteaa aetgagteta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250

tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450 tggatcccca gcagctggtg ctcactcact gaaggtcctg agtgtgatgt 500 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750 gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800 tgacccaat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850

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<220> <223> Synthetic oligonucleotide probe

<210> 356 <211> 50 <212> DNA <213> Artificial Sequence

<400> 355 ccaggtcggg taaggatggt tgag 24





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<210> 358 <211> 328 <212> PRT <213> Homo sapiens

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Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu 215 220 225 Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser 230 235 240 Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile 255 245 250 Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg 270 260 265 Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser 275 280 285 Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg 290 295 300 Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro 305 310 315 Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg 320 325 <210> 359 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 359 tctgctgagg tgcagctcat tcac 24 <210> 360 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 360 gaggctctgg aagatctgag atgg 24



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<210> 361 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 362 <211> 3038 <212> DNA <213> Homo sapiens

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taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363 <211> 500 <212> PRT <213> Homo sapiens

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Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr 20 25 30

Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu 35 40 45

Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn 50 55 60

Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln 65 70 75

Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val 80 85 90

Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp 95 100 105

Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu 110 115 120

Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln 125 130 135

Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His 140 145 150

Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys 155 160 165

Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly170175180

Cys Ala Ile Asn Leu Cys His Asn Met Asn Ile Trp Gly Gln Ile

Trp Pro Lys Ala Val Tyr Leu Val Cys Asn Tyr Ser Pro Lys Gly Asn Trp Trp Gly His Ala Pro Tyr Lys His Gly Arg Pro Cys Ser Ala Cys Pro Pro Ser Phe Gly Gly Gly Cys Arg Glu Asn Leu Cys Tyr Lys Glu Gly Ser Asp Arg Tyr Tyr Pro Pro Arg Glu Glu Glu Thr Asn Glu lle Glu Arg Gln Gln Ser Gln Val His Asp Thr His Val Arg Thr Arg Ser Asp Asp Ser Ser Arg Asn Glu Val Ile Ser Ala Gln Gln Met Ser Gln Ile Val Ser Cys Glu Val Arg Leu Arg Asp Gln Cys Lys Gly Thr Thr Cys Asn Arg Tyr Glu Cys Pro Ala Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro

Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg

410 415 420

Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr 425 430 435

Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His 440 445 450

Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro 455 460 465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile 470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg 485 490 495

Val Phe Ala Val Val 500

<210> 364 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 364 ggacagaatt tgggagcaca ctgg 24

<210> 365 <211> 20 <212> DNA <213> Artificial Sequence

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<400> 365 ccaagagtat actgtcctcg 20

<210> 366 <211> 25 <212> DNA

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<400> 369

<210> 369 <211>1685 <212> DNA <213> Homo sapiens

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<220> <223> Synthetic oligonucleotide probe

<210> 368 <211>50 <212> DNA

<213> Artificial Sequence

aaccactcca gcatgtactg ctgc 24

<220> <223> Synthetic oligonucleotide probe

<210> 367 <211>24

<213> Artificial Sequence

<400> 366 agcacagatt ttctctacag ccccc 25

<223> Synthetic oligonucleotide probe

<213> Artificial Sequence

<220>

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<400> 367

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gaacatgcag tactaaagca atatatttgt gattccccat gtaattcttc 1450 aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgcgccc 1500 tttcctctgt acatataccc ttaagaacgc cccctccaca cactgccccc 1550 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370 <211> 111 <212> PRT <213> Homo sapiens

<400> 370 Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu 1 5 10 15

Leu Ala Ala Leu Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala 20 25 30

Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys 35 40 45

Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr505560

Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val 65 70 75

Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln 80 85 90

Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys 95 100 105

Arg Arg Val Tyr Glu Glu 110

<210> 371 <211> 22 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 371 cagcgccctc cccatgtccc tg 22

<210> 372 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 372 tcccaactgg tttggagttt tccc 24

<210> 373 <211> 45 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 373 ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374 <211> 3113 <212> DNA <213> Homo sapiens

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acceteattg acagecaage acagtateea gttgteaaea caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cacccccac tggagagagg 250

cggtttcagc ccccagaacc cccgtcctcc tggactggca tccgaaatac 300 tactcagttt gctgctgtgt gcccccagca cctggatgag agatccttac 350 tgcatgacat gctgcccatc tggtttaccg ccaatttgga tactttgatg 400 acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450 gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500 gtaatgaccg tggtgaagac gaagatattc atgatcagaa cagtaagaag 550 cccgtcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600 catgattgac ggcagcattt tggcaagcta cggaaacgtc atcgtgatca 650 ccattaacta ccgtctggga atactagggt ttttaagtac cggtgaccag 700 gcagcaaaag gcaactatgg gctcctggat cagattcaag cactgcggtg 750 gattgaggag aatgtgggag cctttggcgg ggaccccaag agagtgacca 800 tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850 cactactcag aaggtetett ccagaaggee atcattcaga geggeacege 900 cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950 tggcagacaa ggtcggctgc aacatgctgg acaccacgga catggtagaa 1000 tgcctgcgga acaagaacta caaggagctc atccagcaga ccatcacccc 1050 ggccacctac cacatagcct tcgggccggt gatcgacggc gacgtcatcc 1100 cagacgaccc ccagatcctg atggagcaag gcgagttcct caactacgac 1150 atcatgctgg gcgtcaacca aggggaaggc ctgaagttcg tggacggcat 1200 cgtggataac gaggacggtg tgacgcccaa cgactttgac ttctccgtgt 1250 ccaacttcgt ggacaacctt tacggctacc ctgaagggaa agacactttg 1300 cgggagacta tcaagttcat gtacacagac tgggccgata aggaaaaccc 1350 ggagacgcgg cggaaaaccc tggtggctct ctttactgac caccagtggg 1400

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taagagactt tgt 3113

<210> 375 <211> 816 <212> PRT <213> Homo sapiens

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Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val 80 85 90

Cys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu 95 100 105

Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val 110 115 120

Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn lle Tyr Val Pro 125 130 135

Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr140145150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser 155 160 165

Lys Lys Pro Val Met Val Tyr lle His Gly Gly Ser Tyr Met Glu 170 175 180

Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly 185 190 195

Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly 200 205 210

Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu 215 220 225

Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly 230 235 240

Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly 245 250 255

Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser 260 265 270

Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu 275 280 285

Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile 290 295 300

- Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met 305 310 315
- Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln320325330
- Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile335340345
- Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln 350 355 360
- Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly 365 370 375
- Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly 380 385 390
- Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp 395 400 405
- Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr 410 415 420
- Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu 425 430 435
- Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp 440 445 450
- Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser 455 460 465
- Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met 470 475 480
- Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr 485 490 495
- Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys500505510
- Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr 515 520 525

- Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val530535540
- Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu 545 550 555
- Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu 560 565 570
- His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr 575 580 585
- Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu 590 595 600
- Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Lys Val Pro Pro 605 610 615
- Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala 620 625 630
- Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn 635 640 645
- Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp 650 655 660
- Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu665670675
- Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile 680 685 690
- Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His 695 700 705
- Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp710715720
- Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys 725 730 735
- Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp 740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg755760765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr 770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe 785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly 800 805 810

His Ser Thr Thr Arg Val 815

<210> 376 <211> 25 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

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<210> 377 <211> 25 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 377 aacccccgag ccaaaagatg gtcac 25

<210> 378 <211> 47 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe <400> 379 gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50 ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100 ttgttggggt ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150 cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200 gcacaggcag tteeteactg tggaatetga tgggcaatge catggtgatg 250 acccagtata tccgccttac cccagatatg caaagtaaac agggtgcctt 300 gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg caggtgcact 350 tcaaaatcca tggacaagga aagaagaatc tgcatgggga tggcttggca 400 atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450 ggacaaattt gtggggctgg gagtatttgt agacacctac cccaatgagg 500 agaagcagca agagcgggta ttcccctaca tctcagccat ggtgaacaac 550 ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600 aggetgeaca gecattgtee geaatettea ttaegacaee tteetggtga 650 ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700 catgagtgga gggactgcat tgaagtgccc ggagtccgcc tgccccgcgg 750 ctactacttc ggcacctcct ccatcactgg ggatctctca gataatcatg 800 atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850 gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

<210> 379
<211> 2461

<212> DNA

<213> Homo sapiens

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<400> 380

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Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala lle Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val

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Arg Phe Tyr

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<210> 382 <211> 24 <212> DNA <213> Artificial Sequence

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<400> 382 cactetecag getgeatget cagg 24

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<210> 384 <211> 3150 <212> DNA <213> Homo sapiens

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Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro505560

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu 65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser 80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val 95 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala110115120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His 125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser 140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu 155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu170175180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp 185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr 200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe 215 220 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe 230 235 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu 245 250 255 Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln 260 265 270

Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro 275 280 285

Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys290295300

His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys 305 310 315

Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu 320 325 330

Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser 335 340 345

Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met 350 355 360

Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr 365 370 375

Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly 380 385 390

Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe 395 400 405

Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg 410 415 420

Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys425430435

Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu 440 445 450

Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly 455 460 465

Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe 470 475 480



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<400> 386 ccaagcagct tagagctcca gacc 24

<210> 387 <211> 25 <212> DNA <213> Artificial Sequence

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<400> 387 ttccctatgc tctgtattgg catgg 25

<210> 388 <211> 50 <212> DNA <213> Artificial Sequence

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<400> 388 gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389 <211> 3313 <212> DNA <213> Homo sapiens

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gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200 cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250 gtatgtggaa acaacggagg agetetgaet teceaactgt eccattetat 300 gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350 aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400 aaagggcttg tcctgctggg aatcctcctg gggactctgt gggagaccgg 450 atgcacccag atacgctatt cagttccgga agagctggag aaaggctcta 500 gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550 gagcgcggag tccgcatcat ccccagaggt aggacgcagc ttttcgccct 600 gaatccgcgc agcggcagct tggtcacggc gggcaggata gaccgggagg 650 agetetgtat gggggceate aagtgteaat taaatetaga cattetgatg 700 gaggataaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750 cgacaatgcg ccttactttc gtgaaagtga attagaaata aaaattagtg 800 aaaatgcagc cactgagatg cggttccctc taccccacgc ctgggatccg 850 gatatcggga agaactetet geagagetae gageteagee egaacaetea 900 cttctccctc atcgtgcaaa atggagccga cggtagtaag taccccgaat 950 tggtgctgaa acgcgccctg gaccgcgaag aaaaggctgc tcaccacctg 1000 gtccttacgg cctccgacgg gggcgacccg gtgcgcacag gcaccgcgcg 1050 catccgcgtg atggttctgg atgcgaacga caacgcacca gcgtttgctc 1100 agcccgagta ccgcgcgagc gttccggaga atctggcctt gggcacgcag 1150 ctgcttgtag tcaacgctac cgaccctgac gaaggagtca atgcggaagt 1200 gaggtattcc ttccggtatg tggacgacaa ggcggcccaa gttttcaaac 1250 tagattgtaa ttcagggaca atatcaacaa taggggagtt ggaccacgag 1300 🚽

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Gly Asp Ile Ser Arg Asp Leu Gly Leu Glu Pro Arg Glu Leu Ala 50 55 60

Glu Arg Gly Val Arg Ile Ile Pro Arg Gly Arg Thr Gln Leu Phe 65 70 75

Ala Leu Asn Pro Arg Ser Gly Ser Leu Val Thr Ala Gly Arg Ile 80 85 90

Asp Arg Glu Glu Leu Cys Met Gly Ala Ile Lys Cys Gln Leu Asn 95 100 105

Leu Asp Ile Leu Met Glu Asp Lys Val Lys Ile Tyr Gly Val Glu 110 115 120

Val Glu Val Arg Asp Ile Asn Asp Asn Ala Pro Tyr Phe Arg Glu 125 130 135

Ser Glu Leu Glu Ile Lys Ile Ser Glu Asn Ala Ala Thr Glu Met 140 145 150

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Ser Leu Gln Ser Tyr Glu Leu Ser Pro Asn Thr His Phe Ser Leu 170 175 180

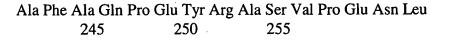
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Leu Lys Arg Ala Leu Asp Arg Glu Glu Lys Ala Ala His His Leu 200 205 210

Val Leu Thr Ala Ser Asp Gly Gly Asp Pro Val Arg Thr Gly Thr 215 220 225

Ala Arg Ile Arg Val Met Val Leu Asp Ala Asn Asp Asn Ala Pro 230 235 240





- Ala Leu Gly Thr Gln Leu Leu Val Val Asn Ala Thr Asp Pro Asp 260 265 270
- Glu Gly Val Asn Ala Glu Val Arg Tyr Ser Phe Arg Tyr Val Asp 275 280 285
- Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr 290 295 300
- Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr305310315
- Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg 320 . 325 330
- Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro 335 340 345
- Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser 350 355 360
- Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp 365 370 375
- Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu 380 385 390
- Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val 395 400 405
- Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile410415420
- Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu425430435
- Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro440445450
- Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn 455 460 465

- Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp 470 475 480
- Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr 485 490 495
- Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp500505510
- Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe515520525
- Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro 530 535 540
- Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln 545 550 555
- Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp 560 565 570
- Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly 575 580 585
- Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln 590 595 600
- Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly 605 610 615
- Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg 620 625 630
- Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala 635 640 645
- Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu 650 655 660
- Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu665670675
- Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr 680 685 690

Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu 695 700 705

- Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His 710 715 720
- Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala 725 730 735
- Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu 740 745 750
- Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys 755 760 765
- Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val 770 775 780
- Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Ser Gly 785 790 795
- Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser 800 805 810
- Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser 815 820 825
- Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln 830 835 840
- Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn845850855
- Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr860865870
- Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu Leu 875 880 885
- Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp 890 895 900
- Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro 905 910 915



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<400> 392 ctcgggcgca ttgtcgttct ggtc 24

<210> 393 <211> 40 <212> DNA <213> Artificial Sequence

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<400> 394 cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggetecaga ategtgtace aggeagagaa etgaagtaet 100

Ala

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150 ctggaagacc tcaccatggg acgcccccga cctcgtgcgg ccaagacgtg 200 gatgtteetg etettgetgg ggggageetg ggeaggaeae teeagggeae 250 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300 tggcaggcgg ccttgttcca gggccagcaa ctactctgtg gcggtgtcct 350 tgtaggtggc aactgggtcc ttacagctgc ccactgtaaa aaaccgaaat 400 acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450 caagaaatac ctgtggttca gtccatccca cacccctgct acaacagcag 500 cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550 aggcatecet ggggtecaaa gtgaageeea teageetgge agateattge 600 acccagcetg gecagaagtg cacegtetea ggetggggea etgteaccag 650 tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700 ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750 atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800 tggaggcccc ctggtgtgtg atggtgcact ccagggcatc acatcctggg 850 gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900 tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950 ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395 <211> 260 <212> PRT <213> Homo sapiens

<400> 395 Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu 1 5 10 15 Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu 20 25 30

Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro 35 40 45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly 50 55 60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys 65 70 75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn 80 85 90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro 95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp 110 115 120

Leu Met Leu Cln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys 125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln 140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu 155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro 170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln lle Thr Asp Gly 185 190 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly 200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile 215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly 230 235 240 Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile 245 250 255

Ile Gly Ser Lys Gly 260

<210> 396 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 396 cagcctacag aataaagatg gccc 24

<210> 397 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 397 ggtgcaatga tctgccaggc tgat 24

<210> 398 <211> 48 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 398 agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399 <211> 2236 <212> DNA <213> Homo sapiens

<400> 399

ggcgccggtg caccgggcgg gctgagcgcc tcctgcggcc cggcctgcgc 50 gecceggece gecgecge ceaegecea acceggece gegeceeta 100 gcccccgccc gggcccgcgc ccgcgcccgc gcccaggtga gcgctccgcc 150 ggaaccgggc ggatteeteg egegteaaac eacetgatee eataaaacat 250 tcatcctccc ggcggcccgc gctgcgagcg ccccgccagt ccgcgccgcc 300 gccgccctcg ccctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350 cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400 gggccggggc cgggccgtag cggcggcgcc tggatgcgga cccggccgcg 450 gggagacggg cgcccgcccc gaaacgactt tcagtccccg acgcgccccg 500 cccaacccct acgatgaaga gggcgtccgc tggagggagc cggctgctgg 550 catgggtgct gtggctgcag gcctggcagg tggcagcccc atgcccaggt 600 gcctgcgtat gctacaatga gcccaaggtg acgacaagct gcccccagca 650 gggcctgcag gctgtgcccg tgggcatccc tgctgccagc cagcgcatct 700 tcctgcacgg caaccgcatc tcgcatgtgc cagctgccag cttccgtgcc 750 tgccgcaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800 tgatgcggct gccttcactg gcctggccct cctggagcag ctggacctca 850 gcgataatgc acageteegg tetgtggace etgecacatt ceaeggeetg 900 ggccgcctac acacgctgca cctggaccgc tgcggcctgc aggagctggg 950 cccggggctg ttccgcggcc tggctgccct gcagtacete tacetgcagg 1000 acaacgcgct gcaggcactg cctgatgaca ccttccgcga cctgggcaac 1050 ctcacacacc tcttcctgca cggcaaccgc atctccagcg tgcccgagcg 1100 cgccttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150

gcgtggccca tgtgcacccg catgccttcc gtgaccttgg ccgcctcatg 1200 acactetate tgtttgccaa caatetatea gegetgecea etgaggeeet 1250 ggcccccctg cgtgccctgc agtacctgag gctcaacgac aacccctggg 1300 tgtgtgactg ccgggcacgc ccactctggg cctggctgca gaagttccgc 1350 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400 tgacctcaaa cgcctagctg ccaatgacct gcagggctgc gctgtggcca 1450 ccggccctta ccatcccatc tggaccggca gggccaccga tgaggagccg 1500 ctggggcttc ccaagtgctg ccagccagat gccgctgaca aggcctcagt 1550 actggagcct ggaagaccag cttcggcagg caatgcgctg aagggacgcg 1600 tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650 aatgactcac cctttgggac tctgcctggc tctgctgagc ccccgctcac 1700 tgcagtgcgg cccgagggct ccgagccacc agggttcccc acctcgggcc 1750 ctcgccggag gccaggctgt tcacgcaaga accgcacccg cagccactgc 1800 cgtctgggcc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850 ctcaggtgcc ctacccagcc tcacctgcag cctcaccccc ctgggcctgg 1900 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000 ccgccaagcc agccgggcgg ccgacccgtg gggcaggcca ggccaggtcc 2050 tccctgatgg acgcctgccg cccgccaccc ccatctccac cccatcatgt 2100 ttacagggtt cggcggcagc gtttgttcca gaacgccgcc tcccacccag 2150 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210>400

<211> 473 <212> PRT <213> Homo sapiens

<400> 400 Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val 1 5 10 15

Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala 20 25 30

Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln 35 40 45

Gln Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln 50 55 60

Arg Ile Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala 65 70 75

Ser Phe Arg Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser 80 85 90

Asn Val Leu Ala Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala 95 100 105

Leu Leu Glu Gln Leu Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser 110 115 120

Val Asp Pro Ala Thr Phe His Gly Leu Gly Arg Leu His Thr Leu 125 130 135

His Leu Asp Arg Cys Gly Leu Gln Glu Leu Gly Pro Gly Leu Phe 140 145 150

Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr Leu Gln Asp Asn Ala 155 160 165

Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp Leu Gly Asn Leu 170 175 180

Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser Val Pro Glu185190195

Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu Leu His

Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro lle Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly

425 430 435

Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu 440 445 450

Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val 455 460 465

Leu Trp Thr Val Leu Gly Pro Cys 470

<210> 401 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 401 tggctgccct gcagtacctc tacc 24

<210> 402 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 402 ccctgcaggt cattggcagc tagg 24

<210> 403 <211> 45 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 403 aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210>404

<400>404 ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50 ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100 agecteagat actggggaet ttacagteee acagaacegt ecteeaga 150 agetgaatee ageaagaaca atggaggeea gegggaaget catttgeaga 200 caaaggcaag teettttte ettteteett ttgggettat etetggeggg 250 cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300 cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350 tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400 gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450 aggatetgtg eggteacaea gageeetgtg tgetaegttt ceaagtgttg 500 ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550 aaacgaccac tctccagtat ttctggacaa acaaatgttg gtgaaagtat 600 cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650 ttagatgtag gccaaaacaa tattgagaac tatataatca gccccaactc 700 ctattttcgg gtcctcaccc gcaaacgcag tgatggcagg aaatacccag 750 agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800 ttaacactca cagcactgga tggtggctct ccgcccagat ctggcactgc 850 tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900 agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950 ctggttgtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000

<211> 2738 <212> DNA <213> Homo sapiens



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ctcctggtgg acggcttete ecagecetae etgeetetee eggaggegge 2200 cccgaeceag geceaggeeg acttgeteae egtetaeetg gtggtggegt 2250 tggeetegg gtettegete tteetettt eggtgeteet gttegtggeg 2300 gtgeggetgt gtaggaggag eagggeggee teggtgggte getgettggt 2350 geeegaggge eccetteeag ggeatettgt ggaeatgage ggeaeeagga 2400 ceetateeea gagetaeeag tatgaggtgt gtetggeagg aggeteaggg 2450 accaatgagt teaagtteet gaageegatt atceeeaaet teeeteeea 2500 gtgeeetggg aaagaaatae aaggaaatte taeetteeea aataaetttg 2550 ggtteaatat teagtgaeea tagttgaett ttaeatteea taggtatttt 2600 attttgtgge attteeatge eaatgtttat tteeeeaat ttgtgtgtat 2650 gtaatattgt acggattae tettgatttt teteatgtte ttteteett 2700 tgttttaaag tgaacattta eetttattee tggttett 2738

<210> 405 <211> 798 <212> PRT <213> Homo sapiens

<400>405 Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu 15 1 5 10 Phe Ser Phe Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu 20 25 30 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe 45 35 40 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe 60 50 55 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His 65 70 75

Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Asn Glu Lys Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly Thr Ala Gln Val Tyr lle Glu Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Glu Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp Ser Pro Val Gly Phe Leu Val Val Lys Val Ser Ala Thr Asp Val Asp Thr Gly Val Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala Ser Glu Glu Ile Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly

Glu Ile Glu Leu Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser305310315

Tyr Glu Val Asn Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly 320 325 330

Lys Cys Thr Val Leu Ile Gln Val Ile Asp Val Asn Asp His Ala 335 340 345

Pro Glu Val Thr Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn 350 355 360

Ala Pro Glu Thr Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp 365 370 375

Ser Gly Glu Asn Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu 380 385 390

Pro Phe Leu Leu Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr 395 400 405

Glu Arg Pro Leu Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr 410 415 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu425430435

Asn Met Thr Val Leu Ile Ala Asp Val Asn Asp Asn Ala Pro Ala 440 445 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser 455 460 465

Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser 470 475 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp 485 490 495

Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn 500 505 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln 515 520 525

- Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala 530 535 540
- Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn 545 550 555
- Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala 560 565 570
- Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu 575 580 585
- Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala 590 595 600
- Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe 605 610 615
- Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu 620 625 630
- Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys 635 640 645
- Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val 650 655 660
- Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu 665 670 675
- Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu 680 685 690
- Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val 695 700 705
- Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala 710 715 720
- Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His 725 730 735
- Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln 740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys 755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly 770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe 785 790 795

Asn Ile Gln

<210> 406 <211> 23 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 406 ctgagaacgc gcctgaaact gtg 23

<210> 407 <211> 22 <212> DNA <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407 agcgttgtca ttgacatcgg cg 22

<210> 408 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 408 ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50 <400>409 acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100 cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200 agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250 ggctgtgtac ctgggtgagg aggagctcct gcatgacccg atgggccagg 300 acagggcagc agaagaggcć aatgcggtgc tggggctgga cacccaaggc 350 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500 cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550 atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650 actctgaaaa ttttaaatat gtcacaggac cttatggatt ttctgaaccc 700 aaacggtagt gactgtactc tagtcctgtt ttacaccccg tggtgccgct 750 tttctgccag tttggcccct cactttaact ctctgccccg ggcatttcca 800 caggtttggc accgtagctg ttcctaatat tttattattt caaggagcta 900 aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950 atcttcattt ttaatcagac aggtatagaa gccaagaaga atgtggtggt 1000

<210> 409 <211> 1379 <212> DNA

<213> Homo sapiens

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<210> 410 <211> 360 <212> PRT <213> Homo sapiens

<400>410 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu 10 1 5 15 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val 20 25 30 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu 35 40 45 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly 50 55 60 Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala 65 70 75 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His 80 85 90 Met Val Met Leu Ser Val Ile Pro Gly Glu Ala Glu Asp Lys Val 95 100 105 Ser Ser Glu Pro Ser Gly Val Thr Cys Gly Ala Gly Gly Ala Glu 110 115 120

Asp Ser Arg Cys Asn Val Arg Glu Ser Leu Phe Ser Leu Asp Gly 125 130 135

Ala Gly Ala His Phe Pro Asp Arg Glu Glu Glu Tyr Tyr Thr Glu 140 145 150

Pro Glu Val Ala Glu Ser Asp Ala Ala Pro Thr Glu Asp Ser Asn 155 160 165

Asn Thr Glu Ser Leu Lys Ser Pro Lys Val Asn Cys Glu Glu Arg 170 175 180

Asn Ile Thr Gly Leu Glu Asn Phe Thr Leu Lys Ile Leu Asn Met 185 190 195

Ser Gln Asp Leu Met Asp Phe Leu Asn Pro Asn Gly Ser Asp Cys 200 205 210

Thr Leu Val Leu Phe Tyr Thr Pro Trp Cys Arg Phe Ser Ala Ser215220225

Leu Ala Pro His Phe Asn Ser Leu Pro Arg Ala Phe Pro Ala Leu 230 235 240

His Phe Leu Ala Leu Asp Ala Ser Gln His Ser Ser Leu Ser Thr 245 250 255

Arg Phe Gly Thr Val Ala Val Pro Asn Ile Leu Leu Phe Gln Gly260265270

Ala Lys Pro Met Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu 275 280 285

Thr Leu Lys Ile Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys290295300

Lys Asn Val Val Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro 305 310 315

Ser Thr Leu Ile Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu 320 325 330

Phe Phe Leu Ile Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu 335 340 345





Ser Ile Arg Trp Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu 350 355 360

<210> 411 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 411 cacagagcca gaagtggcgg aatc 24

<210> 412 <211> 25 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 412 ccacatgttc ctgctcttgt cctgg 25

<210> 413 <211> 45 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 413 cggtagtgac tgtactctag tcctgtttta caccccgtgg tgccg 45

<210> 414 <211> 1196 <212> DNA <213> Homo sapiens

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Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro lle Pro Val 35 40 45

Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu 50 55 60

Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln 65 70 75

Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp 80 85 90

Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp95100105

Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln 110 115 120

Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro 125 130 135

Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp140145150

Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr 155 160 165

Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp 170 175 180

Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala 185 190 195

Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr

200 205 210

Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn 215 220 225

Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys 230 235 240

Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala 245 250 255

Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile 260 265 270

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Thr Ile Cys Leu Trp Glu Ser Val Pro Pro Thr Pro Pro Ser Ala Gly Ala Ala Ser Ser Thr Ser Glu Lys Phe Leu Asp Gly Leu Lys Leu Gln Leu Met Trp Asn Lys Ala Tyr Val Ile Leu Ala Val Cys Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp Thr Val Ser Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser

Cys lle Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln 440 445 450 Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly 455 460 465 Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala 480 470 47.5 Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg 485 490 495 Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro 500 505 510 Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr 515 520 525 Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala 530 535 540 Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser 545 550 555 Pro Trp Val Ile Thr 560 <210> 421 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400>421 agetteteag eccetetgga geag 24 <210>422 <211>25 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe

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Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg505560

Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu 65 70 75

Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg 80 85 90

Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu95100105

Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His 110 115 120

Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe 125 130 135

Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu 140 145 150

Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys 285· His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro

Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro 605 610 615

- Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala 620 625 630
- Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His 635 640 645
- Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val 650 655 660
- Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile665670675
- Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu 680 685 690
- Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser 695 700 705
- Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile 710 715 720
- Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu 725 730 735
- Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr 740 745 750
- Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg 755 760 765
- Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val 770 775 780
- Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His 785 790 795
- Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro 800 805 810
- Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr 815 820 825

- Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu 830 835 840
- Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln 845 850 855
- Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro860865870
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- Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His 905 910 915
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- Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu 935 940 945
- Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Val Gln 950 955 960
- Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln 965 970 975
- Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly 980 985 990
- Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg 995 1000 1005
- Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp 1010 1015 1020
- Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu 1025 1030 1035
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Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala 1145 1150 1155

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Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser 35 40 45

Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe505560

Glu lle Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp 65 70 75

Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val 80 85 90

Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu 95 100 105

His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe 110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser 125 130 135

Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val 140 145 150

- Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly 160 165 155 Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn 175 180 170 Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln 185 190 195 Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met Ala 205 210 200 Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser 220 225 215 Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly 235 240 230 Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu 245 250 255
- Glu Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala 260 265 270
- Thr Lys Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr275280285
- Phe Asn Phe Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys 290 295 300
- Ile Phe Met Ala Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys 305 310 315
- Thr Asp Pro Val Thr Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu320325330
- Gly Ile Gln Phe Asp Val Lys Phe Trp Ser Gln His Ile Ser Phe 335 340 345
- Ile Leu Val Gly Ile Ile Ile Val Thr Ser Ile Arg Gly Leu Leu350355360
- Ile Thr Leu Thr Lys Phe Phe Tyr Ala Ile Ser Ser Lys Ser365370375

Ser Asn Val Ile Val Leu Leu Leu Ala Gln Ile Met Gly Met Tyr 380 385 390

Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser Met Pro Leu Glu 395 400 405

Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu Gln Phe Asn 410 415 420

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Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala Val Leu Gly Asp Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val



Gly Ala Pro Phe Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly 410 415 420

Ser Ser Leu Gly Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly 425 430 435

Glu Ala Val Gly Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser 440 445 450

Leu Asp Met Asp Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser 455 460 465

Leu Ala Asp Thr Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His 470 475 480

Val Ser His Glu Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu 485 490 495

Gln Pro Asn Cys Ala Gly Gly His Ser Val Cys Val Asp Leu Arg 500 505 510

Val Cys Phe Ser Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr 515 520 525

Val Ala Leu Asp Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu 530 535 540

Arg Gly Gln Val Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu 545 550 555

Glu Pro Lys His Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln 560 565 570

His Asp Arg Val Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn 575 580 585

Val Lys Asp Lys Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser 590 595 600

Leu Gln Thr Pro Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu 605 610 615

Pro Pro Val Ala Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln 620 625 630

Arg Ala Glu Ile His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys Ile Cys Gln Ser Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr Arg Val Ser Asp Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp Gly Thr Thr Ala Leu Phe Ala Leu Ser Gly Gln Pro Val Ile Gly 685 · Leu Glu Leu Met Val Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr Glu Leu Glu Val Glu Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser-Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln

- Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro 860 865 870
- His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val 875 880 885
- Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser 890 895 900
- Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg 905 910 915
- Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu920925930
- Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu 935 940 945
- Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn 950 955 960
- Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala 965 970 975
- Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu 980 985 990
- Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn 995 1000 1005
- Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala101010151020
- Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val 1025 1030 1035
- Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu 1040 1045 1050
- Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Trp Lys 1055 1060 1065
- Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro 1070 1075 1080

Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe 1085 1090 1095

Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser 1100 1105 1110

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Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu 35 40 45

Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys505560

Phe Arg Asp Glu Val Glu Asp Asp Tyr Phe Arg Thr Trp Ser Pro 65 70 75

Gly Lys Pro Phe Asp Gln Ala Leu Asp Pro Ala Lys Asp Pro Cys 80 85 90

Leu Lys Met Lys Cys Ser Arg His Lys Val Cys Ile Ala Gln Asp 95 100 105

Ser Gln Thr Ala Val Cys Ile Ser His Arg Arg Leu Thr His Arg 110 115 120

Met Lys Glu Ala Gly Val Asp His Arg Gln Trp Arg Gly Pro Ile 125 130 135

Leu Ser Thr Cys Lys Gln Cys Pro Val Val Tyr Pro Ser Pro Val 140 145 150

Cys Gly Ser Asp Gly His Thr Tyr Ser Phe Gln Cys Lys Leu Glu 155 160 165

Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser Val Lys Cys Glu 170 175 180

Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser Thr Ser Arg 185 190 195

Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu Val Ala

Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly Ser

Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp Met Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln Ser Glu Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr Lys Ala Phe Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile Ser Asn Asn Glu Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro Pro Cys Gln Thr Glu Leu Ser Asn Ile Gln Lys Arg Gln Gly Val Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly 335 . Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn · 365 Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr

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<223> Synthetic oligonucleotide probe

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<210> 444 <211> 28 <212> DNA <213> Artificial Sequence

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<210> 447 <211> 229 <212> PRT <213> Homo sapiens

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Glu Cys Phe Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile 50 55 60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His 65 70 75

Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys 80 85 90

Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met 95 100 105

Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile 110 115 120

Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu 125 130 135

Gln Glu Asp Trp Lys Lys Tyr lle Thr Gly Thr Asp lle Leu Asp 140 145 150

Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser 155 160 165 Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe 170 175 180

Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val 185 190 195

Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser 200 205 210

Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg 215 220 225

Lys Ser Arg Thr

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<220> <223> Synthetic oligonucleotide probe

<400> 448 cccagcaggg ctgggcgaca aga 23

<210> 449 <211> 23 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 449 gtcttccagt ttcatatcca ata 23

<210> 450 <211> 43 <212> DNA <213> Artificial Sequence

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<400> 451 ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

<210> 451 <211> 859 <212> DNA <213> Homo sapiens

<400> 450 ccagaaggag cacggggaag ggcagccaga tcttgtcgcc cat 43 <210> 452 <211> 175 <212> PRT <213> Homo sapiens

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Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln 20 25 30

Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys 35 40 45

Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser 50 55 60

Trp Met Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro Ser Gly Lys 65 70 75

Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val Ser Ser 80 85 90

Leu Val Arg Ser Ile Ser Asn Ser Tyr Ser Tyr Ile Trp Ile Gly 95 100 105

Leu His Asp Pro Thr Gln Gly Ser Glu Pro Asp Gly Asp Gly Trp 110 115 120

Glu Trp Ser Ser Thr Asp Val Met Asn Tyr Phe Ala Trp Glu Lys 125 130 135

Asn Pro Ser Thr Ile Leu Asn Pro Gly His Cys Gly Ser Leu Ser 140 145 150

Arg Ser Thr Gly Phe Leu Lys Trp Lys Asp Tyr Asn Cys Asp Ala 155 160 165

Lys Leu Pro Tyr Val Cys Lys Phe Lys Asp 170 175

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<210> 454 <211> 125 <212> PRT <213> Homo sapiens

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Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro 80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro 95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu 110 115 120

Leu Ser Leu Arg Leu 125

<210> 455 <211> 1518 <212> DNA <213> Homo sapiens

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Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val 50 55 60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln 65 70 75

Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu808590

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp 95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg 110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn 125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile 140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu 155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His 170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys185190195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys 200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg 215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly 230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser 245 250 255 Asn Ser Ser Arg Leu His Thr Cys Gln Arg His 260 265

<210> 457 <211> 638 <212> DNA <213> Homo sapiens

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attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaa 4040

<210> 459 <211> 747 <212> PRT <213> Homo sapiens

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Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly

 65
 70
 75

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met 195 . 190 -Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn

		•			•
2	290	295	300		
	sp Phe Glu La 305	eu Leu Ser Ala 310	a Asn Thr Leu Glu 315	u Asp Arg	
	is His Arg Tr 320	p Leu Leu Phe 325	Phe His Phe Gly 330	' Lys Asn	
	er Asn Asp P 335	ro Glu Leu Ly 340	s Lys Leu Lys Th 345	r Leu Leu	
-	sp His Ile Gli 350	n Val Gly Arg 355	Phe Asp Cys Ser 360	Ser Ala	
-	e Cys Ser Ası 365	n Leu Tyr Val 370	Phe Gln Pro Ser I 375	Leu Ala	
-	ys Gly Gln G 380	ly Thr Lys Glu 385	Tyr Glu Ile His I 390	His Gly	
	e Leu Tyr Asj 395	o Ile Leu Ala P 400	Phe Ala Lys Glu S 405	Ser Val	
	is Val Thr Th 410	rr Leu Gly Pro 415	Gln Asn Phe Pro 420	Ala Asn	
	ilu Pro Trp Le 425	eu Val Asp Pho 430	e Phe Ala Pro Trp 435	o Cys Pro	
-	rg Ala Leu La 440	eu Pro Glu Leu 445	ו Arg Arg Ala Sei 450	r Asn Leu	
•	ly Gln Leu Ly 455	ys Phe Gly Th 460	r Leu Asp Cys Th 465	r Val His	
•	eu Cys Asn N 470	fet Tyr Asn lle 475	e Gln Ala Tyr Pro 480	Thr Thr	
	ne Asn Gln Se 485	er Asn Ile His 490	Glu Tyr Glu Gly 495	His His	
	lu Gln Ile Leu 500	i Glu Phe Ile G 505	Glu Asp Leu Met A 510	Asn Pro	
Ser Val Va	al Ser Leu Th	r Pro Thr Thr I	Phe Asn Glu Leu	Val Thr	

Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp Val Ile Asp Phe Tyr Ala Pro Trp Cys Gly Pro Cys Gln Asn Phe Ala Pro Glu Phe Glu Leu Leu Ala Arg Met Ile Lys Gly Lys Val Lys Ala Gly Lys Val Asp Cys Gln Ala Tyr Ala Gln Thr Cys Gln Lys Ala Gly Ile Arg Ala Tyr Pro Thr Val Lys Phe Tyr Phe Tyr Glu Arg Ala Lys Arg Asn Phe Gln Glu Glu Gln Ile Asn Thr Arg Asp Ala Lys Ala Ile Ala Ala Leu Ile Ser Glu Lys Leu Glu Thr Leu Arg Asn Gln Gly Lys Arg Asn Lys Asp Glu Leu

745

<210> 460 <211> 24 <212> DNA <213> Artificial Sequence

740

<220>

<223> Synthetic oligonucleotide probe

<400> 460 actccccagg ctgttcacac tgcc 24

<210> 461 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 461 gatcagccag ccaataccag cage 24

<210> 462 <211> 50 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 462 gtggtgatga tagaatgett tgccgaatga aaggagteaa cagetateee 50

<210> 463 <211> 1818 <212> DNA <213> Homo sapiens

<400> 463 agacagtacc tcctccctag gactacacaa ggactgaacc agaaggaaga 50

ggacagagca aagccatgaa catcatccta gaaatccttc tgcttctgat 100

caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150 agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200 catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250 attggttctg tgggatatta ataagcgcgg tgtggaggaa actgcagctg 300 agtgccgaaa actaggcgtc actgcgcatg cgtatgtggt agactgcagc 350 aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400 tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgatc 450 ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500 ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550 aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600 ttccttacct catcccatat tgttccagca aatttgccgc tgttggcttt 650 cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700 aacctcatgt ctctgcccag tttttgtgaa tactgggttc accaaaaatc 750 caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850 tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900 cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950 aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000 ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050 tttttcagtc ctgataatat taaaaacatt ggtttggcac tagcagcagt 1100 caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatttac 1150 gtagtttttc ataggtctgt ttttcctttc atgcctctta aaaacttctg 1200 tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250

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<210> 464 <211> 300 <212> PRT <213> Homo sapiens

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Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr 80 85 90

- Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn 95 100 105
- Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn 110 115 120
- Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu 125 130 135
- Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp 140 145 150
- Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly155160165
- His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro 170 175 180
- Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe 185 190 195
- His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly 200 205 210
- Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe215220225
- Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp230235240
- Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys 245 250 255
- Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln 260 265 270
- Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln 275 280 285
- Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys 290 295 300

<400>465 cggcggcggc tgcgggcgcg aggtgagggg cgcgaggtga ggggcgcgag 50 gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccg 100 gagagggccc agcccgcccg gggcaggatg accaaggccc ggctgttccg 150 gctgtggctg gtgctggggt cggtgttcat gatcctgctg atcatcgtgt 200 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250 aggccgcaca cggggccgcc gctgcccacg cccgggccgg acagggacag 300 ggageteacg gccgactecg atgtcgacga gtttetggac aagtttetea 350 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400 cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450 gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550 aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600 cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650 gcaccaactg gaagcgcgtg atgatcgtgc tgagcggaag cctgctgcac 700 cgcggtgcgc cctaccgcga cccgctgcgc atcccgcgcg agcacgtgca 750 caacgccagc gcgcacctga ccttcaacaa gttctggcgc cgctacggga 800 agetetecceg ceaceteatg aaggteaage teaagaagta caceaagtte 850 ctcttcgtgc gcgacccctt cgtgcgcctg atctccgcct tccgcagcaa 900 gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccatgc 950 tgcggctgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000

<210> 465 <211> 1547 <212> DNA <213> Homo sapiens





tteegegetg geeteaaggt gteettegee aaetteatee agtaeetget 1050 ggaeeegeae aeggagaage tggegeeett eaaegageae tggeggeagg 1100 tgtaeegeet etgeeaeeeg tgeeagateg aetaegaett egtggggaag 1150 etggagaete tggaegagga egeeggeag etgetgeage taeteeaggt 1200 ggaeeggeag eteegettee eeeegageta eeggaaeagg aeegeeagea 1250 getgggagga ggaetggtte geeaagatee eeetggeetg gaggeageag 1300 etgtataaae tetaegagge egaetttgtt etettegget aeeeeaagee 1350 eetggaaeete eteegagaet gaaagettte gegttgettt ttetegetg 1400 eetggaaeet gaegeaegeg eaettegtt tttttatgae etaegatttt 1450 geaatetggg ettettgtte aeteeaetge etetateeat tgagtaetgt 1500 ategatattg ttttttaaga ttaatatatt teaggtattt aataega 1547

<210> 466 <211> 414 <212> PRT <213> Homo sapiens

<400> 466

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Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp 95 100 105

- Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln 110 115 120
- Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser 125 130 135
- Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro 140 145 150
- Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala 155 160 165
- Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg170175180
- Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro 185 190 195
- Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala 200 205 210
- Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys 215 220 225
- Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys 230 235 240
- Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe 245 250 255
- Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe 260 265 270
- Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro 275 280 285
- Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe 290 295 300
- Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu 305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His 320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu 335 340 345

Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg 350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser 365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln 380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr 395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp 410

<210> 467 <211> 1071 <212> DNA <213> Homo sapiens

<400>467

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<210> 468 <211> 270 <212> PRT <213> Homo sapiens

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Cys Asp Val Thr Gln Glu Asp Asp Val Lys Thr Leu Val Ser Glu

. . 65 70 75

Thr Ile Arg Arg Phe Gly Arg Leu Asp Cys Val Val Asn Asn Ala Gly His His Pro Pro Pro Gln Arg Pro Glu Glu Thr Ser Ala Gln Gly Phe Arg Gln Leu Leu Glu Leu Asn Leu Leu Gly Thr Tyr Thr Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn Cys lle Ser Pro Gly Asn lle Trp Thr Pro Leu Trp Glu Glu Leu Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser <210>469<211>687 <212> DNA <213> Homo sapiens

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ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470 <211> 180 <212> PRT <213> Homo sapiens

<400> 470 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile 1 5 10 15 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys 20 25 30 Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val 35 40 45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu

Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn 70[.] 75 65 Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu 80 85 90 Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile 95 100 105 Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg 110 115 120 Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp 125 130 135 Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg 150 140 145 Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln 160 165 155 Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe 170 175 180 <210>471 <211>2368 <212> DNA <213> Homo sapiens <400>471 gcgccgccag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50 aaacccggcg ggcgagcgag gctgcgggcc ggccgctgcc cttccccaca 100 ctccccgccg agaagcctcg ctcggcgccc aacatggcgg gtgggcgctg 150

50

55

60

cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200

cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250

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40

35

Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr 50 55 60

45

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu 65 70 75

Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys 80 85 90

Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val 95 100 105

Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg110115120

Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile 125 130 135

Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys 140 145 150

Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser 155 160 165

Ile Ser Gly Lys Ile Trp His Leu His Asn Tyr Phe Thr Val Thr 170 175 180

Leu Gly Ile Pro Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala 185 190 195

Thr Leu Val Phe Gly Leu Phe Met Gly Leu Val Leu Val Val Ile200205210

Ser Glu Cys Phe Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg 215 220 225

Ser Glu Gln Asn Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln 230 235 240 Leu Gln Asp Ala Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu 245 250 255

Asn Lys Asp Ser Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu 260 265 270

Gly Asp Glu Asp Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu 275 280 285

Ala Ala Gly Val Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly 290 295 300

Pro Pro Gly Glu Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu 305 310 315

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Glu Val Glu Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala 335 340 345

Asp Lys Gly Leu

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<210> 474 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 474 ctctcctcat ccacaccagc agcc 24



<210> 475 <211> 44 <212> DNA <213> Artificial Sequence

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<210> 476 <211> 2478 <212> DNA <213> Homo sapiens

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Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro

65 70 75

Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met 80 85 90

Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu 95 100 105

Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe 110 115 120

Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile125130135

Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp 140 145 150

Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala 155 160 165

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Glu Lys Lys Phe Ser Met 200

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<210> 480 <211> 24 <212> DNA <213> Artificial Sequence

<220> <223> Synthetic oligonucleotide probe

<400> 480 atcctcccag agccatggta cctc 24

<210> 481 <211> 51 <212> DNA <213> Artificial Sequence

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His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys 185 (Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr . 365 Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val

Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu

Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe 620 625 630

Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile 635 640 645

Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser650655660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn 665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser 680 685 690

Ser Arg Ile

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<220> <221> unsure

<222> 68, 70, 84, 147 <223> unknown base

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tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450

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<210> 487 <211> 2849 <212> DNA <213> Homo sapiens

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110

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Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala 175. Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly



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His Val Ile Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro 50 55 60

Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn 65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His 80 85 90 Leu Val Glu Ile Asp Phe Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile . 185 Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys

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	Gly Asp Ala Lys F 335	Phe Leu His Phe 340	e Leu Pro Ser Leu Ile Gln 345	Leu		•	
	Asp Leu Ser Phe A 350	Asn Phe Glu Let 355	u Gln Val Tyr Arg Ala Se 360	er Met			
	Asn Leu Ser Gln A 365	Ala Phe Ser Ser 370	Leu Lys Ser Leu Lys lle 375	Leu			
	Arg Ile Arg Gly T 380	yr Val Phe Lys 385	Glu Leu Lys Ser Phe Asr 390	n Leu			
	Ser Pro Leu His A 395	Asn Leu Gln Asi 400	n Leu Glu Val Leu Asp L 405	eu Gly			
	Thr Asn Phe Ile L 410	ys lle Ala Asn 415	Leu Ser Met Phe Lys Gln 420	Phe			
	Lys Arg Leu Lys 425	Val Ile Asp Leu 430	n Ser Val Asn Lys Ile Ser 435	Pro			•
	Ser Gly Asp Ser 5 440	Ser Glu Val Gly 445	Phe Cys Ser Asn Ala Ar 450	g Thr	• •		
	Ser Val Glu Ser 7 455	Гуг Glu Pro Gln 460	Val Leu Glu Gln Leu Hi 465	s Tyr			
	Phe Arg Tyr Asp 470	Lys Tyr Ala Aı 475	rg Ser Cys Arg Phe Lys A 480	sn Lys			
	Glu Ala Ser Phe 485	Met Ser Val As 490	n Glu Ser Cys Tyr Lys Ty 495	yr Gly		•	
	Gln Thr Leu Asp 500	b Leu Ser Lys A 505	sn Ser Ile Phe Phe Val Ly 510	vs Ser			
	Ser Asp Phe Gln 515	His Leu Ser Ph 520	ie Leu Lys Cys Leu Asn I 525	eu Ser			
	Gly Asn Leu Ile 530	Ser Gln Thr Lev 535	u Asn Gly Ser Glu Phe G 540	ln Pro			

. 1

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His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val 785 790 795

Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr 800 805 810

Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val 815 820 825

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Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val845850855

Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile 860 865 870

Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile 875 880 885

Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys 890 895 900

Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys 905 910 915

Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu 920 925 930

Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln 935 940 945

Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys 950 955 960

Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His 965 970 975

Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe 980 985 990 Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys 995 1000 1005

Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln101010151020

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Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly

Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser .340 Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu

Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His Phe Thr Arg Pro Leu lle Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg

Tyr lle Ser lle Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp

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Leu Ser L	eu Asn Arg L	eu Lys His Ile	Pro Asn Glu Ala Phe Leu
	650	655	660
Asn Leu I	Pro Ala Ser Le	eu Thr Glu Leu	u His Ile Asn Asp Asn Met
	665	670	675
Leu Lys P	Phe Phe Asn T	rp Thr Leu Le	u Gln Gln Phe Pro Arg Leu
	680	685	690
Glu Leu I	.eu Asp Leu A	Arg Gly Asn L	ys Leu Leu Phe Leu Thr Asp
	695	700	705
Ser Leu S	er Asp Phe Tl	nr Ser Ser Leu	Arg Thr Leu Leu Leu Ser
	710	715	720
His Asn A	Arg Ile Ser His	s Leu Pro Ser (Gly Phe Leu Ser Glu Val
	725	730	735
Ser Ser L	eu Lys His Le	u Asp Leu Ser	Ser Asn Leu Leu Lys Thr
	740	745	750
Ile Asn L	ys Ser Ala Lei	u Glu Thr Lys	Thr Thr Thr Lys Leu Ser
	755	760	765
Met Leu	Glu Leu His C	Gly Asn Pro Ph	ne Glu Cys Thr Cys Asp Ile
	770	775	780
Gly Asp I	Phe Arg Arg T 785		lu His Leu Asn Val Lys Ile 795
Pro Arg I	eu Val Asp V	al Ile Cys Ala	Ser Pro Gly Asp Gln Arg
	800	805	810
• •	Ser Ile Val Ser	Leu Glu Leu '	Thr Thr Cys Val Ser Asp
	815	820	825
Val Thr A	Ala Val Ile Leu	Phe Phe Phe	Thr Phe Phe Ile Thr Thr
	830	835	840
Met Val I	Met Leu Ala A	Ala Leu Ala Hi	s His Leu Phe Tyr Trp Asp
	845	850	855
Val Trp P	he lle Tyr As	n Val Cys. Leu	Ala Lys Val Lys Gly Tyr

860 865 870

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- Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu 890 895 900
- Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu 905 910 915
- Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp 920 925 930
- Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val 935 940 945
- Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe 950 955 960
- Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile 965 970 975
- Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu 980 985 990
- Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro 995 1000 1005
- Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn 1010 1015 1020
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Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val 35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg 50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg 65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro 80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala 95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro110115120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln 125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln 140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu 155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly 170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala 185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu

200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala 215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu 230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu 245 250 255

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Lys Asp Ser

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Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu . Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp Ser

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Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu 50 55 60

Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu 65 70 75

Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp 80 85 90

Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile 95 100 105

Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln 110 115 120

Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile 125 130 135 Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala

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Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val 35 40 45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp505560

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu 65 70 75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu 80 85 90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val 95 100 105 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr Leu Gin Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val

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Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu 35 40 45

Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro 50 55 60

Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly 65 70 75

Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp 80 85 90

Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu 95 100 105

Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp 110 115 120

Gln Asn Gln Ala lle Leu Lys His Leu Leu Glu Asn Thr Thr Phe 125 130 135

Asn Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu 140 145 150

Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro 155 160 165 Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly

Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile Leu Asn Asn Tyr Leu Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg

Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr 380 385 390 Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala . Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr

Leu Gly Glu Asn Ile Thr Asp Asn Gly Gly Leu Lys Ala Ala Tyr 635 640 645

Asn Ala Tyr Lys Ala Trp Leu Arg Lys His Gly Glu Glu Gln Gln 650 655 660

Leu Pro Ala Val Gly Leu Thr Asn His Gln Leu Phe Phe Val Gly 665 670 675

Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu Ser Ser His680685690

Glu Gly Leu Val Thr Asp Pro His Ser Pro Ala Arg Phe Arg Val 695 700 705

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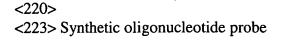
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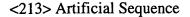
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65 70 75

Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser 80 85 90

Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn95100105

Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr 110 115 120

Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val 125 130 135

Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu 140 145 150

Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu155160165

Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe 170 175 180

Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln 185 190 195

Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro 200 205 210

Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile 215 220 225

Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu 230 235 240

Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe Glu Trp 245 250 255

Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly Ile Ile 260 265 270

Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr Asn Val275280285

Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys

290 295 300

Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro Ser Thr 305 310 315

Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe Ser Cys 320 325 330

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Gly Pro Pro Gly Val Lys Gly Glu Ala Gly Leu Gln Gly Pro Gln Gly Ala Pro Gly Lys Gln Gly Ala Thr Gly Thr Pro Gly Pro Gln Gly Glu Lys Gly Ser Lys Gly Asp Gly Gly Leu Ile Gly Pro Lys Gly Glu Thr Gly Thr Lys Gly Glu Lys Gly Asp Leu Gly Leu Pro Gly Ser Lys Gly Asp Arg Gly Met Lys Gly Asp Ala Gly Val Met Gly Pro Pro Gly Ala Gln Gly Ser Lys Gly Asp Phe Gly Arg Pro Gly Pro Pro Gly Leu Ala Gly Phe Pro Gly Ala Lys Gly Asp Gln Gly Gln Pro Gly Leu Gln Gly Val Pro Gly Pro Pro Gly Ala Val Gly His Pro Gly Ala Lys Gly Glu Pro Gly Ser Ala Gly Ser Pro Gly Arg Ala Gly Leu Pro Gly Ser Pro Gly Ser Pro Gly Ala Thr Gly Leu Lys Gly Ser Lys Gly Asp Thr Gly Leu Gln Gly Gln Gln Gly Arg Lys Gly Glu Ser Gly Val Pro Gly Pro Ala Gly Val Lys Gly Glu Gln Gly Ser Pro Gly Leu Ala Gly Pro Lys Gly Ala Pro Gly Gln Ala Gly Gln Lys Gly Asp Gln Gly Val Lys Gly Ser Ser Gly Glu Gln Gly Val Lys Gly Glu Lys Gly Glu Arg Gly Glu Asn

Ser Val Ser Val Arg Ile Val Gly Ser Ser Asn Arg Gly Arg Ala 430 435 425 Glu Val Tyr Tyr Ser Gly Thr Trp Gly Thr Ile Cys Asp Asp Glu 450 440 445 Trp Gln Asn Ser Asp Ala Ile Val Phe Cys Arg Met Leu Gly Tyr 455 460 465 Ser Lys Gly Arg Ala Leu Tyr Lys Val Gly Ala Gly Thr Gly Gln 475 480 470 Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu 495 490 485 Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His 500 505 510 Glu Glu Asp Ala Gly Val Glu Cys Ser Val 515 520 <210>614 <211>647

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Lys lle Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val 35 40 45

Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp 50 55 60

Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu 65 70 75

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Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser

155 160 165

Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro Asp Arg Tyr Val Ile Leu Gly

Gly His Arg Asp Ser Trp Val Phe Gly Gly Ile Asp Pro Gln Ser

	380	385	390
Gly Ala	Ala Val Val H 395	is Glu Ile Val 400	Arg Ser Phe Gly Thr Leu 405
Lys Lys (Glu Gly Trp A	rg Pro Arg Arg	g Thr Ile Leu Phe Ala Ser
	410	415	420
Trp Asp	Ala Glu Glu P	he Gly Leu Le	u Gly Ser Thr Glu Trp Ala
	425	430	435
Glu Glu	Asn Ser Arg L	eu Leu Gln Gl	u Arg Gly Val Ala Tyr lle
	440	445	450
Asn Ala	Asp Ser Ser Il	e Glu Gly Asn	Tyr Thr Leu Arg Val Asp
	455	460	465
Cys Thr	Pro Leu Met T	yr Ser Leu Va	l His Asn Leu Thr Lys Glu
	470	475	480
Leu Lys	Ser Pro Asp G	lu Gly Phe Glu	u Gly Lys Ser Leu Tyr Glu
	485	490	495
Ser Trp 7	Fhr Lys Lys Se	er Pro Ser Pro	Glu Phe Ser Gly Met Pro
	500	505	510
Arg Ile S	er Lys Leu Gl	y Ser Gly Asn	Asp Phe Glu Val Phe Phe
	515	520	525
Gln Arg	Leu Gly Ile A	la Ser Gly Arg	Ala Arg Tyr Thr Lys Asn
	530	535	540
Trp Glu	Thr Asn Lys P	he Ser Gly Ty	r Pro Leu Tyr His Ser Val
	545	550	555
Tyr Glu '	Thr Tyr Glu L	eu Val Glu Ly:	s Phe Tyr Asp Pro Met Phe
	560	565	570
Lys Tyr I	His Leu Thr V	al Ala Gln Val	Arg Gly Gly Met Val Phe
	575	580	585
Glu Leu	Ala Asn Ser I	e Val Leu Pro	Phe Asp Cys Arg Asp Tyr
	590	595	600
Ala Val Val Leu Arg Lys Tyr Ala Asp Lys The Tyr Ser The Ser			

Ala Val Val Leu Arg Lys Tyr Ala Asp Lys Ile Tyr Ser Ile Ser

605 615 610 Met Lys His Pro Gln Glu Met Lys Thr Tyr Ser Val Ser Phe Asp 620 625 630 Ser Leu Phe Ser Ala Val Lys Asn Phe Thr Glu Ile Ala Ser Lys 635 640 645 Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser Asn Pro Ile Val 660 650 655 Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu Arg Ala Phe 670 675 665 Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val 680 685 690 Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe 700 705 695 Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp 710 715 720 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala 730 735 725 Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala 740 745 750 <210> 618 <211>24 <212> DNA <213> Artificial Sequence <220> <223> Synthetic oligonucleotide probe <400> 618 agatgtgaag gtgcaggtgt gccg 24 <210> 619 <211>25 <212> DNA <213> Artificial Sequence



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<220> <223> Synthetic oligonucleotide probe

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